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OM protein - protein search, using sw model

Run on: July 12, 2001, 17:12:38 ; search time 13.8 seconds  
(without alignments)  
849.578 Million cell updates/sec

Title: US-09-294-539-4

Perfect score: 2952

Sequence: 1 MEPPTSHTVNAFSDSDASV.....RSLGSSSSSTSGAIRPRR 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 193259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1276	43.2	593	2	US-08-989-478-2
2	1276	43.2	593	3	US-08-996-685-2
3	1276	43.2	593	3	US-08-880-179-3
4	1270	43.0	593	2	US-08-989-478-8
5	1270	43.0	593	3	US-08-996-685-8
6	1188.5	40.3	521	2	US-08-989-478-12
7	1188.5	40.3	521	3	US-08-996-685-12
8	1134	38.4	469	2	US-08-989-478-10
9	1134	38.4	469	3	US-08-996-685-10
10	1052.5	35.7	397	2	US-08-989-478-14
11	1052.5	35.7	397	3	US-08-996-685-14
12	751	25.4	261	2	US-08-989-478-16
13	751	25.4	261	3	US-08-996-685-16
14	133	4.5	1088	4	US-09-082-059-2
15	127	4.3	1839	2	US-09-172-977-4
16	126	4.3	843	2	US-09-172-977-3
17	124.5	4.2	300	2	US-08-897-340-32
18	124.5	4.2	300	4	US-09-252-329-32
19	122	4.1	41	2	US-08-989-478-17
20	122	4.1	41	2	US-08-989-478-19
21	122	4.1	41	2	US-08-989-478-21
22	122	4.1	41	2	US-08-989-478-23
23	122	4.1	41	3	US-08-996-685-17
24	122	4.1	41	3	US-08-996-685-19
25	122	4.1	41	3	US-08-996-685-21
26	122	4.1	41	3	US-08-996-685-23
27	122	4.1	41	3	US-08-880-179-4

28	122	4.1	41	3	US-08-880-179-6	Sequence 6, Appl1
29	122	4.1	41	3	US-08-880-179-8	Sequence 8, Appl1
30	122	4.1	41	3	US-08-880-179-10	Sequence 10, Appl1
31	119.5	4.0	359	1	US-08-388-756-2	Sequence 2, Appl1
32	119.5	4.0	359	2	US-08-748-428-2	Sequence 2, Appl1
33	119.5	4.0	359	2	US-08-802-322-3	Sequence 3, Appl1
34	119.5	4.0	389	2	US-08-802-322-14	Sequence 14, Appl1
35	116	3.9	787	4	US-09-188-930-334	Sequence 334, Appl1
36	111.5	3.8	356	2	US-08-903-851-2	Sequence 2, Appl1
37	110	3.7	418	2	US-08-978-182-5	Sequence 5, Appl1
38	110	3.7	418	2	US-09-205-681-5	Sequence 5, Appl1
39	110	3.7	1745	2	US-09-031-485-33	Sequence 33, Appl1
40	110	3.7	1745	2	US-08-847-429A-33	Sequence 33, Appl1
41	110	3.7	1745	3	US-09-065-474-33	Sequence 33, Appl1
42	108	3.7	969	1	US-08-365-689-3	Sequence 3, Appl1
43	108	3.7	969	1	US-07-747-781-3	Sequence 3, Appl1
44	108	3.7	969	1	US-08-145-138A-3	Sequence 3, Appl1
45	108	3.7	969	5	PCT-US92-06888-3	Sequence 3, Appl1

## ALIGNMENTS

RESULT 1

US-08-989-478-2

; Sequence 2: Application US/08989478

; Patent No. 5986082

; GENERAL INFORMATION:

; APPLICANT: Uknes, Scott

; APPLICANT: Hunt, Michelle

; APPLICANT: Steiner, Henry-York

; APPLICANT: Ryals, John

; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING

; NUMBER OF INVENTIONS: DISEASE RESISTANCE IN PLANTS

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5986082artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: No. 5986082th Carolina

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30.

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/989,478

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/033,177

; FILING DATE: 13-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,379

; FILING DATE: 27-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,382

; FILING DATE: 27-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/034,730

; FILING DATE: 10-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/035,021

; FILING DATE: 10-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/035,022

; FILING DATE: 10-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: PF/5-21214/PI/CGC1911

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 593 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-478-2

Query Match 43.2%; Score 1276; DB 2; Length 593;

Best Local Similarity 47.2%; Pred. No. 1.le-121;  
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNFAFSDSDASVEGDADADVEALRRLLSDNLAARFSPEDFAFLADARIAVPGG 64  
DB 17 TSVFATDNTDSSIVVLAEEQVLTGPDVSALQLLSNFSFVDSFDD--FYSDAKLVL--- 71  
QY 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAGGGGDSERLELRLGGGEEVEVG 124  
DB 72 -SDGREVSFHRVLSARSFPLRGVFAARRAAAGGGGDSERLELRLGGGEEVEVG 124  
QY 125 YEALRLVLDLYSGRVGDLPAKACLCVDECAHVCHPAVAFMAQVLPAASTFQVAELTN 184  
DB 125 FDSVTVLAIVYSSRRPPKGVSCADENCHVACRAVDFMELVLYLAFIKPIELIT 184  
QY 185 LQORLLDVLKVEVDNLLLSVANLCKNSCKMLLECLDCLMVRNSLDMITLESIPPD 244  
DB 185 LYORHLDDVVKVIEDTLVILKLANICGKACMKLLDRCKEIIIVKSNVDMVLSKSLPEE 244  
QY 245 VIKQITDARLSLGLSPENKGNPKHVRIRHRLSDSDVDELVRMLLTGOTNLDLDAFALH 304  
DB 245 LVKEIIDRKLGLGKVPKVK---KHSNVHRLSDSDVDELVRMLLTGOTNLDLDAFALH 300  
QY 305 YAVEHCDSTKTTLLDLALADVNHPRGYTVLHIAARREPKIIVSLTKGARPDVTF 364  
DB 301 FAVAYCNVKTATDLKLDLADVNHPRGYTVLHIAARREPKIIVSLTKGARPDVTF 360  
QY 365 DGRKAVOISRLTKQDYGVTGEGPSPKDLICILILQEAERROPOLGEASVSLAMAGE 424  
DB 361 EGRALMIAQATMAVECNIPQCKHSLKGLCVLEIQEDKREQIPDRVPPSPFAVAD 420  
QY 425 SLGRLLYLNENVALARIMPEARVAMDAQVDGTFLEFNLAGSGANPPPP---QRTTV 480  
DB 421 ELKMTLLDENRVALAQLPTEAQAAMEIAEMKGTCEFIVTS---LEPDRLTGKRTSP 477  
QY 481 DLNESPFIKKEHLARMTALSKTVELGKFPFRCNSVLDKIMD--DETDPVSLGRDTSAEK 539  
DB 478 GVKIAPFRILEEHQSRKLSKTVELGKFPFRCNSVLDKIMD--DETDPVSLGRDTSAEK 537  
QY 540 R-----KRFHLDVLOKAFHDEKENDRSLSSSSSTS 574  
DB 538 RLQKKRYMEIQETLKAFFEDNLELGNLSLTSTSTS 576

RESULT 2  
US-08-996-685-2  
Sequence 2, Application US/08996685.  
Patent No. 6031153  
GENERAL INFORMATION:  
APPLICANT: Ryals, John  
APPLICANT: Friedrich, Leslie  
APPLICANT: Uknes, Scott  
APPLICANT: Molina, Antonio  
APPLICANT: Ruess, Wilhelm  
APPLICANT: Knauf-Beiter, Gertrude  
APPLICANT: Kung, Ruth  
APPLICANT: Kessmann, Helmut  
APPLICANT: Oostendorp, Michael  
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6031153artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6031153th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/996.685  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/761,543  
FILING DATE: 6-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,378  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,379  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,382  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,730  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,021  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,022  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,024  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/875,015  
FILING DATE: 16-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 593 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-996-685-2

Query Match 43.2%; Score 1276; DB 3; Length 593;

Best Local Similarity 47.2%; Pred. No. 1.le-121;  
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNFAFSDSDASVEGDADADVEALRRLLSDNLAARFSPEDFAFLADARIAVPGG 64  
DB 17 TSVFATDNTDSSIVVLAEEQVLTGPDVSALQLLSNFSFVDSFDD--FYSDAKLVL--- 71  
QY 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAGGGGDSERLELRLGGGEEVEVG 124  
DB 72 -SDGREVSFHRVLSARSFPLRGVFAARRAAAGGGGDSERLELRLGGGEEVEVG 124  
QY 125 YEALRLVLDLYSGRVGDLPAKACLCVDECAHVCHPAVAFMAQVLPAASTFQVAELTN 184

Db 125 FDSVTVLAYVYSSRVPPKGVSECADENCCHVACRPVAFDMFLVLYLAFIKFIPELIT 184  
QY 185 LFQRRLLDVKVEVDNLLILSVANLCKSKMKLLERCLDMVVRNLDMLITLKSLLPPD 244  
Db 185 LYQRLHLLDVVKKVIEDTLVILKLANICGKACMKLLDRCKEIIIVSNVDMVSLKSLPEE 244  
QY 245 VIKQIIDARLSGLISPENKGFNKHVRRIHRLALSDDDVELVRLMLTETGOTNLDLDAFALH 304  
Db 245 LVKEIIDRRKELGLEVPVKV---KHVSNVHKAALSDDDIELVKLLKEDHTNLDLDAFALH 300  
QY 305 YAVEHCOSKITTELLDLALADVNHPRGYTVLHIAARREPKIIVSLTGTGARPADVTF 364  
Db 301 FAVAYCNVATATDLLKLDLADVNHPRGYTVLHVAARKEPKIIVSLTGTGARPADVTF 360  
QY 365 DGRKAVQISKRLTKQDYGFTVEEGKPSKDRLCIELEQAERDPPQJLGEASVSLAMAGE 424  
Db 361 EGTALMIKATMAVECNIPQCKHSLKGRCLVCEIQEDKREQIPRDVPPSFVAAD 420  
QY 425 SLRGLLYLENVALARIMFPMEARVAMDTAQVDGTLEFNLGSGANPPPER---QRTTV 480  
Db 421 ELKMTLLDLLENVALAQLRFPTEAQAAMEIAEMKGTCEFTVTS---LEPDLRTGTRTSP 477  
QY 481 DLNESPFIKKEHARMTALSKTVELGKRPFCNSVNLKIMD-DETDVPVSLGRDTSK 539  
Db 478 GVKIAPFRILEEHQSRKALKSKTVELGKRPFCNSVNLKIMD-DETDVPVSLGRDTSK 537  
QY 540 R---KRFHDLQDVLOKAFHEKEDNDRSGLSLSSSSSTS 574  
Db 538 RLQKKORYMEIQETLKKAFSEDNLELGNSSLTDTSTS 576

RESULT 3

US-08-880-179-3  
; Sequence 3, Application US/08880179

; Patent No. 6091004

; GENERAL INFORMATION:

; APPLICANT: Ryals, John

; APPLICANT: Delaney, Terry

; APPLICANT: Friedrich, Leslie

; APPLICANT: Weymann, Kristiana

; APPLICANT: Lawton, Kay

; APPLICANT: Ellis, Daniel

; APPLICANT: Uknes, Scott

; APPLICANT: Jesse, Taco

; APPLICANT: Vos, Pieter

; TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE

; TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESIS

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6091004artis Corporation

; STREET: 520 White Plains Road, P.O. Box 2005

; CITY: Tarrytown

; STATE: New York

; COUNTRY: USA

; ZIP: 10591

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/880,179

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: CGC 1909

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919) 541-8587

; TELEFAX: (919) 541-8689

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 593 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-880-179-3

Query Match 43.28; Score 1276; DB 3; Length 593;  
Best Local Similarity 47.2%; Pred. No. 1.1e-121;  
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSDSASVEEGDADADADVEALRRSLDNLAAAFRSPEDFAFLADARIAVPGG 64  
Db 17 TSEVATDNTDSSIVYLAEEQVLTGPDVSAQLLSNFSFVDSFDD--FSDAKLVL--- 71  
QY 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAAGGGGDSERLELELGGGEEVEVG 124  
Db 72 -SDGREVSFHRCVLSARSFPLRGVFAARRAAAAGGGGDSERLELELGGGEEVEVG 124  
QY 125 YEALRLVLDLYISGRVGDLPKAAACLCVDECAHVGHCHPAVAFMAQVLFASSTFQVAVELTN 184  
Db 125 FDSVTVLAYVYSSRVPPKGVSECADENCCHVACRPVAFDMFLVLYLAFIKFIPELIT 184  
QY 185 LFQRRLLDVKVEVDNLLILSVANLCKSKMKLLERCLDMVVRNLDMLITLKSLLPPD 244  
Db 185 LYQRLHLLDVVKKVIEDTLVILKLANICGKACMKLLDRCKEIIIVSNVDMVSLKSLPEE 244  
QY 245 VIKQIIDARLSGLISPENKGFNKHVRRIHRLALSDDDVELVRLMLTETGOTNLDLDAFALH 304  
Db 245 LVKEIIDRRKELGLEVPVKV---KHVSNVHKAALSDDDIELVKLLKEDHTNLDLDAFALH 300  
QY 305 YAVEHCOSKITTELLDLALADVNHPRGYTVLHIAARREPKIIVSLTGTGARPADVTF 364  
Db 301 FAVAYCNVATATDLLKLDLADVNHPRGYTVLHVAARKEPKIIVSLTGTGARPADVTF 360  
QY 365 DGRKAVQISKRLTKQDYGFTVEEGKPSKDRLCIELEQAERDPPQJLGEASVSLAMAGE 424  
Db 361 EGTALMIKATMAVECNIPQCKHSLKGRCLVCEIQEDKREQIPRDVPPSFVAAD 420  
QY 425 SLRGLLYLENVALARIMFPMEARVAMDTAQVDGTLEFNLGSGANPPPER---QRTTV 480  
Db 421 ELKMTLLDLLENVALAQLRFPTEAQAAMEIAEMKGTCEFTVTS---LEPDLRTGTRTSP 477  
QY 481 DLNESPFIKKEHARMTALSKTVELGKRPFCNSVNLKIMD-DETDVPVSLGRDTSK 539  
Db 478 GVKIAPFRILEEHQSRKALKSKTVELGKRPFCNSVNLKIMD-DETDVPVSLGRDTSK 537  
QY 540 R---KRFHDLQDVLOKAFHEKEDNDRSGLSLSSSSSTS 574  
Db 538 RLQKKORYMEIQETLKKAFSEDNLELGNSSLTDTSTS 576

RESULT 4

US-08-989-478-8

; Sequence 8, Application US/08989478

; Patent No. 5986082

; GENERAL INFORMATION:

; APPLICANT: Uknes, Scott

; APPLICANT: Hunt, Michelle

; APPLICANT: Steiner, Henry-York

; APPLICANT: Ryals, John

; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING

; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5986082artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: No. 5986082th Carolina

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

Thu Jul 12 18:51:25 2001

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/989,478  
FILING DATE: 27-DEC-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 60/033,177  
FILING DATE: 13-DEC-1996  
PRIOR APPLICATION DATA: US 60/034,379  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA: US 60/034,382  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA: US 60/034,730  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA: US 60/035,021  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA: US 60/035,022  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-21214/PL/CGC1911  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 593 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-478-8

Query Match 43.0%; Score 1270; DB 2; Length 593;  
Best Local Similarity 47.0%; Pred. No. 4.6e-121;  
Matches 272; Conservative 113; Mismatches 166; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSASVEEGDADADAEALRLRLSDNLAAFRSPEDFAFLADARTAVPGG 64  
DB 17 TSFVATDNTDSSIVYLAEEQVLGTPDVSALQLLSNFEAVFDAPDD--FYSDAKVLV--- 71  
QY 65 GGGGDLRVHRCVLSARSPLRGVFAARRAAAAGGGEDGSERLRELLGGGEEVEVG 124  
DB 72 -SDGREVFHRCVLSARSFESKALA--AAKKEKDSNNTAAVKLEKEI----AKDVEVG 124  
QY 125 YEALRLVLDLYSGRGVLDLPAACLVDEDCAHVGHCPAVAFMAQVLFRASTFQVAELTN 184  
DB 125 FDSVTVLAYVYSSRVPPKGVSECADENCCHVACRPVDFMLEVLYLAFIKPELIT 184  
QY 185 LFQRLLDVLDKVDNLLILSVANLCNCKMGLERCLDMVRSNLDMLTLEKSLPPD 244  
DB 185 LYQRHLDDVVDKVVITLVILKIANICGKACMKLLDRCKEIIIVKSNVDMVLSLESPPEE 244  
QY 245 VIKOIIDARLSGLISPENKGFPMKXVRIHRAALSDSDVELVRLMLTTEGOTNLDLAFALH 304  
DB 245 LVKEIIDRKLGLVPEVKV---KHVSNNVHKALSDSDIELVKLLKEDHTNLDLACALH 300  
QY 305 YAVEHCOSKITTELDLADLVNDRNPRGTYLVHIAARRREPKTIIVSLTKGARPADVTF 364  
DB 301 FAVAYCNVKTATDLKLDLVNDRNPRGTYLVHVAARRKEPQLITLSLEKGSASATL 360  
QY 365 DGRVAQISKRLTKGDFVGYTEGKPSPKDRLCIELEQAERDPPQLGEASVSLAMAGE 424  
DB 361 EGRTALMTAKATWAVECANNIPEQCKHSLKGLRCLVEILEQEDKREQIPROVPPSFAVAAD 420

QY 425 SLRGRLLYLENVALARIMFPMEARVAMDAOVDGTFLENLGSGANPPPP---QRTTV 480  
DB 421 ELKMTLLDLENVALAQLRFFPEAQAAEMIAEMKGTCEFIYTS---LEPDLRTGTRTSP 477  
QY 481 DLNESPFIKMEHRLAMTALSKTVELGKRFPRCSNVLDKIMD-DETPVSVLGRDTSAEK 539  
DB 478 GYKIAFPRILEEHSRLKALSKTVELGKRFPRCSNVLDKIMD-DETPVSVLGRDTSAEK 537  
QY 540 R----KRFHDLQDVLOKAFHEDKEENDRSGLSSSSSTS 574  
DB 538 RLOKQRYMEIQETLKAFSEDNLGNLSLDTDSSTS 576  
RESULT 5  
US-08-996-685-8  
Sequence 8, Application US/08996685  
Patent No. 6031153  
GENERAL INFORMATION:  
APPLICANT: Ryals, John  
APPLICANT: Friedrich, Leslie  
APPLICANT: Uknes, Scott  
APPLICANT: Molina, Antonio  
APPLICANT: Ruess, Wilhelm  
APPLICANT: Knauf-Beiter, Gertrude  
APPLICANT: Kessmann, Helmut  
APPLICANT: Oostendorp, Michael  
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6031153artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6031153th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/996,685  
FILING DATE: 27-DEC-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 08/761,543  
FILING DATE: 6-DEC-1996  
PRIOR APPLICATION DATA: US 60/034,378  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA: US 60/034,379  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA: US 60/034,382  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA: US 60/034,730  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA: US 60/035,021  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA: US 60/035,022  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA: US 60/035,024  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA: US 08/875,015  
FILING DATE: 16-JUL-1997



ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 541-8587  
 TELEFAX: (919) 541-8689  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 593 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-996-685-8

Query Match 43.0%; Score 1270; DB 3; Length 593;  
 Best Local Similarity 47.0%; Pred. No. 4.6e-12;  
 Matches 272; Conservative 113; Mismatches 166; Indels 28; Gaps 9;

QY 5 TSHVTNFAFSDSDSASVEEGDADADVEALRLSDNLAAFRSPEDFAFLADARIAVPGG 64  
 Db. 17 TSFVATDNTDSIVYLAAEQVLTGPDVSALQLLSNFSFEVDFAPDD--FYSDAKLVL--- 71  
 QY 65 GGGGGLRVHRCVLSARSFPLRGVFAARRAAAGGGGDSERLELRELLGGGEEVEVG 124  
 Db. 72 -SDGREVSFHRVLSARSFFKSALA--AAKKEKDSNNTAAVKLEKEI---AKDYEVG 124  
 QY 125 YEALRLVLDYLYSGRVGDLPLKACLCVDECAHVGHCHPAVAFMAQVLFPAASTFOVAELTN 184  
 Db. 125 FDSVTVLAIVYSSVRPPPKGVSECADENCCHVACRPADVDFMLEVLYLAFIKIPELIT 184  
 QY 185 LFQRLDLDVLDKVEVDNLLILSVANLCNCKMKLLERCLDMVRSNLDMLTLEKSLPPD 244  
 Db. 185 LYQRHLDDVVDKVVIEDTLVILKLANICGKCKMLDRCKEIIIVKSNVDMVLSLESLPEE 244  
 QY 245 VIKQIIDARLSGLISPENKGFNKHVRRIHRLDSDDDVELVRLMLTTEGOTNLDDAFALH 304  
 Db. 245 LVKEIIDRRKELGLEVPVKV---KHVSNVHKALSDSDIELVKLLKEDHTNLDACALH 300  
 QY 305 YAVEHCDSKITTELDLALADVNNHPRGYTVLHIAARREPKIIVSLITKGARPADVTF 364  
 Db. 301 FAVAYCNVATDLDLADVNNHPRGYTVLHVAAMKEPQLILSLLEKASASEATL 360  
 QY 365 DGRKAVOISKRLTKQDYGTVTEEGSPKDRCLCIIEQAERRDPOLGEASVSLSAMAGE 424  
 Db. 361 EGRALMIKQATMAVECNINPEQCKHSLKGLCVLEIQEDKREQIPRDVPPSFAVAD 420  
 QY 425 SLRGLLYLENVALARIMFPMEARVAMDIAQVDGTLFNLGSGANPPPP---ORTTV 480  
 Db. 421 ELKMTLLENVALAQLRPTPEAQAAMEIAEMKGTCEFTVTS---LEPDRLTGKRTSP 477  
 QY 481 DLNESFFIMKEEHLARMTALSKTVLKGKFFPPRCNSVNLKIND--DETDPVSLGRDTSAEK 539  
 Db. 478 GVKIAPFRLEEHQSLKSLKTVLKGKFFPPRCNSAVLDQIMNCEDLTQLACGEDTAEK 537  
 QY 540 R-----KRFHDQDLQKAFHEKDEKNDKRSSSSSSTS 574  
 Db. 538 RLQKORYMEIQETLKAQFSEDNLELGNLSLTDSTSTS 576

RESULT 6  
 US-08-989-478-12  
 Sequence 12, Application US/08989478  
 Patent No. 5986082  
 GENERAL INFORMATION:  
 APPLICANT: Uknes, Scott  
 APPLICANT: Hunt, Michelle  
 APPLICANT: Steiner, Henry-York  
 APPLICANT: Ryals, John  
 TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING  
 TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS  
 NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 5986082artis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: No. 5986082th Carolina  
 COUNTRY: USA  
 ZIP: 27709  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/989,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/033,177  
 FILING DATE: 13-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,379  
 FILING DATE: 27-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,382  
 FILING DATE: 27-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,730  
 FILING DATE: 10-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/035,021  
 FILING DATE: 10-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/035,022  
 FILING DATE: 10-JAN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 541-8587  
 TELEFAX: (919) 541-8689  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 521 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-989-478-12

Query Match 40.3%; Score 1188.5; DB 2; Length 521;  
 Best Local Similarity 48.0%; Pred. No. 7.9e-113;  
 Matches 251; Conservative 100; Mismatches 149; Indels 23; Gaps 7;  
 QY 5 TSHVTNFAFSDSDSASVEEGDADADVEALRLSDNLAAFRSPEDFAFLADARIAVPGG 64  
 Db. 17 TSFVATDNTDSIVYLAAEQVLTGPDVSALQLLSNFSFEVDFAPDD--FYSDAKLVL--- 71  
 QY 65 GGGGGLRVHRCVLSARSFPLRGVFAARRAAAGGGGDSERLELRELLGGGEEVEVG 124  
 Db. 72 -SDGREVSFHRVLSARSFFKSALA--AAKKEKDSNNTAAVKLEKEI---AKDYEVG 124  
 QY 125 YEALRLVLDYLYSGRVGDLPLKACLCVDECAHVGHCHPAVAFMAQVLFPAASTFOVAELTN 184  
 Db. 125 FDSVTVLAIVYSSVRPPPKGVSECADENCCHVACRPADVDFMLEVLYLAFIKIPELIT 184  
 QY 185 LFQRLDLDVLDKVEVDNLLILSVANLCNCKMKLLERCLDMVRSNLDMLTLEKSLPPD 244  
 Db. 185 LYQRHLDDVVDKVVIEDTLVILKLANICGKCKMLDRCKEIIIVKSNVDMVLSLESLPEE 244  
 QY 245 VIKQIIDARLSGLISPENKGFNKHVRRIHRLDSDDDVELVRLMLTTEGOTNLDDAFALH 304  
 Db. 245 LVKEIIDRRKELGLEVPVKV---KHVSNVHKALSDSDIELVKLLKEDHTNLDACALH 300

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; FILING DATE: 10-JAN-1997
; PRIORITY NUMBER: 8
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 521 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-996-685-12

Query Match          40.3%; Score 1188.5; DB 3; Length 521;
Best Local Similarity 48.0%; Pred. No. 7.9e-113;
Matches 251; Conservative 100; Mismatches 149; Indels 23; Gaps

QY      5 TSHVTNAPSDDSASVEEGDADADVAELRRLSDNLAAAFSPEDFLADARIAPGG 64
       || | | : | | | : | | | : | | | : | | | : | | | :
DB      17 TSFTVATNDTSIVYLAAEQVLGPDVSALQLLSNSFESVDFDSPD--FYSDAKLVL--- 71
       || | | : | | | : | | | : | | | : | | | : | | | :

QY      65 GGGGGDLRHRCVLSARSPLRGVFARRAAAAGGGGEDGSERLELRLLGGGGEVEVG 124
       || | | : | | | : | | | : | | | : | | | : | | | :
DB      72 -SDGREVSFHRCVLSARSSFFKSALA--AAKKEKDSNNNTAAYKLKET----AKDYEVG 124
       || | | : | | | : | | | : | | | : | | | : | | | :

QY      125 YEALRLVDLYISGRYCDLPKAACLCVEDCAHVGHCHPAVAPMAOVLFAASTFOVAELTN 184
       : : : : | | | | | | | | | | | | | | | | | | | | | | :
DB      125 FDSVTVTAVYSSRRPPPKGVSECADNCCHVACRPADVFMLEVLYLAFTFKIPELIT 184
       : : : : | | | | | | | | | | | | | | | | | | | | | | :

QY      185 LFQRRLLDVLDKYDEVNDLLILSVANLCKNSCHKMLLERCLDMVVRSLNDMTLEKSLPPD 244
       : : : : | | | | | | | | | | | | | | | | | | | | | | :
DB      185 LYQRHLLDVVDKVIEDTLVLTKLANICGKACMKLDRCKEIIIVKSNVDMVSKSLPEE 244
       : : : : | | | | | | | | | | | | | | | | | | | | | | :

QY      245 VIKQIDARLSGLGISPENKGFNFKHVRIRTHRALDSDDDVELYRMILLTEGOTNLDDAFALH 304
       : | | | : | | | : | | | : | | | : | | | : | | | :
DB      245 LVKEIIDRRKLEGLVEPKVK-----KHVSNVHKALDSDDIELVKLLLKEDHTNLDACALH 300
       : | | | : | | | : | | | : | | | : | | | : | | | :

QY      305 YAVEHCDSKITTELLDALADVNHRNPGRGYTVLIHIAARRREPKIIVSLTKGARPADVTF 364
       : | | | : | | | : | | | : | | | : | | | : | | | :
DB      301 FAVAYCNVKTATDLLKLDADVNRNPRGYTVLHVAAARKKEPOLILSLLEKGASASEATL 360
       : | | | : | | | : | | | : | | | : | | | : | | | :

QY      365 DGRKAVOISRKLTKQGDYFGVTEGFRPSKDRLCIETLEQAERRDPOLCEASVSLAMAGE 424
       : | | | : | | | : | | | : | | | : | | | : | | | :
DB      361 EGRTALMIAQATMAVECNNIPEOCKHSKLGRLUCEILEQEDAKREQIPRDVPSPFAVAAD 420
       : | | | : | | | : | | | : | | | : | | | : | | | :

QY      425 SLRGLRIYLENRVALARIMFPMEARVAMDIAQVDGTLEFNGLSGANGPPPER-----ORTTV 480
       : | | | : | | | : | | | : | | | : | | | : | | | :
DB      421 ELKWTTLDLENRVALARLPTETAQAAMEIAEMKGCEFIWTS--LEPDLRTGTRKTPS 477
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QY      481 DLNESPFIMKEEHARLTALSKTVELGKRFFPCRSNVLDKIMD 523
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DB      478 GVKIAPFRILEHQSRALKSKTVELGKRFFPCRSAYILDQIMN 520
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RESULT      8
US-08-989-478-10
; Sequence 10, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF INVENTIONS: 32

```

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5986082artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: No. 5986082th Carolina  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,478  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/033,177  
; FILING DATE: 13-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,379  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,382  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,730  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,021  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,022  
; FILING DATE: 10-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Melgs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 541-8587  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 469 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-989-478-10

Query Match 38.4%; Score 1134; DB 2; Length 469;  
Best Local Similarity 51.4%; Pred. No. 2.5e-107;  
Matches 233; Conservative 89; Mismatches 115; Indels 16; Gaps 5;  
QY 131 VLDYLSGRVGDLPKAAACLVDECAHVGCHPAVAFMAQVLAASFOVAELNLFQRL 190  
Db 7 VLAYVYSSRVPPKGVSECADENCCVACRPAYDFMFLVLYLAFKIPILITLQRLH 66  
QY 191 LDVLDKVEVDNLLILSVANLCKNSCKMLERCLDMVRSNLDMLTEKSLPPDVIKQII 250  
Db 67 LDVVVKVIEDTLVLKLANICGKACMLDRCKEIIKVSNDVMVSLKSLPEELVKELI 126  
QY 251 DARLSGLISPNKGNPKHVRIRHRLSDSDVVELVPMLLTEGQTNLDDAFALHYAVEHC 310  
Db 127 DRKELGLEVPKVK----KHVSNVHKALEDSDIELVKLLKEDHTNDDACALHFAVAYC 182  
QY 311 DSKITTELLDALADNVNHRNPRGYTVLHIAARRREPKIIVSLTKGARPAVDVFDGRKAV 370  
Db 183 NVATDGLKLDADNVNHRNPRGYTVLHVAAMRKEPQLIISLLEKASASEATLEGTAL 242  
QY 371 QISKRLTKQDVGTVTEEGKSPKDRCLCTEILEQAERRDPQOLGEASVSLAMAGESLRGL 430  
Db 243 MIAKQATMAVECNIPQCKHSLKGLRCVLEIQEDKREQIPRDVPPSFAVADELKMTL 302

QY 431 LVLENVALARIMFMEARVAMDIQVGTLEFNLGSGANPPPP---ORTTVDLNESE 486  
Db 303 LDLENVALAQRLEFTEAQAAMEIAEMKGTCEIVTS---LEPDRLTGKRTSPGVKIAP 359  
QY 487 FIMKEEHLARMTALSKTVELGKRRFFRCNSNVLDKIMD-DETDVPSVGLRDTSAEKR---K 541  
Db 360 FRILEEHQSRKALKSKTVELGKRRFFRCNSAVLDQINNCEDLTQACGEDDTAEKRLQKKQ 419  
QY 542 RFHDLQDVLOKAFHEDKEENDRSGLSSSSSSSTS 574  
Db 420 RYMEIQETLKAFSEDNLELGNLSLTDSTSTS 452  
RESULT 9  
US-08-996-685-10  
; Sequence 10, Application US/08996685  
; Patent No. 6031153  
; GENERAL INFORMATION:  
; APPLICANT: Rvals, John  
; APPLICANT: Friedrich, Leslie  
; APPLICANT: Uknes, Scott  
; APPLICANT: Molina, Antonio  
; APPLICANT: Ruess, Wilhelm  
; APPLICANT: Knauf-Beiter, Gertrude  
; APPLICANT: Kung, Ruth  
; APPLICANT: Kessmann, Helmut  
; APPLICANT: Oostendorp, Michael  
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6031153artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: No. 6031153th Carolina  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,685  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/761,543  
; FILING DATE: 6-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,378  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,379  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,382  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,730  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,021  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,022  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,024  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/875,015  
; FILING DATE: 16-JUL-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-21215/PL/CGC1912  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 469 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-996-685-10

Query Match 38.4%; Score 1134; DB 3; Length 469;  
Best Local Similarity 51.4%; Pred. No. 2.5e-107;  
Matches 233; Conservative 89; Mismatches 115; Indels 16; Gaps 5;  
QY 131 VLDYLYSGRVGDLAKAACLCVDEDCAHVGHCPAVAFMAQVLFPAASTFOVAELTNLFQRL 190  
Db 7 VLAYVYSSRVPPKGVSECADENCHVACRPVDFMLEVLYLAFIFKIPELITLYQRHL 66  
QY 191 LDVLDKVEVDNLLILSVANLCKSCMKLLERCLDMVYRSNLDMTITLESPLPPDVIKQII 250  
Db 67 LDVVDKVVIEDTLVILKLANICGKACMKLLDRCKEIIIVKSNVDVMSLEKSLPEELVKEII 126  
QY 251 DARLSGLISPENKGFPPKRVHRIHRALDSDDELVRMLLTGEGTNLDDAFALHYAVEHC 310  
Db 127 DRKELGLEVPVKV----KHVSNVHKALDSDDELVRMLLTGEGTNLDDAFALHYAVEHC 182  
QY 311 DSKITTELDLADLVNHRNPGYTVLHIAARRPKIIVSLTGTGARPADVTDFGRKAV 370  
Db 183 NVKATDLDLADLVNHRNPGYTVLHIAARRPKIIVSLTGTGARPADVTDFGRKAV 242  
QY 371 QISKRLTKGQDYGVEEGKPSKDLCEILEQAEERDPQGEASVSLAMAGESLGRGL 430  
Db 243 MIAKQATMAVECNIPQCKHSLKGLRCVLEIQEDKEQIPRDVPPSPFAVADELKMTL 302  
QY 431 LYLENRVALARIMFPMEARVAMDIQVDTGLEFNIGSGANPPPER----QRTVDLNEP 486  
Db 303 LDLENRVALAQRLEPTEAQAAMEIAEMKGTCEFIVTS---LEPDRLTGTGRTSPGVKIAP 359  
QY 487 FIMKEEHLARMTALSKTVELGKRFPPRCNSVLDKIMD-DETDPVSLGRDTSAEKR----K 541  
Db 360 FRILEEHQSRKALKSKTVELGKRFPPRCNSAVLDQIMNCEDLTLQACGEDDTAEKRLQKKQ 419  
QY 542 RFHDLQVLOKAFHEKDEKNDKSLSSSSSTS 574  
Db 420 RYMEIQETLAKAFSEDNLELGNLSLTDSTS 452

RESULT 10  
US-08-989-478-14  
Sequence 14, Application US/08989478  
Patent No. 5986082  
GENERAL INFORMATION:  
APPLICANT: Ukes, Scott  
APPLICANT: Hunt, Michelle  
APPLICANT: Steiner, Henry-York  
APPLICANT: Ryals, John  
TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING  
DISEASE RESISTANCE IN PLANTS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5986082artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 5986082th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/989,478  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/033,177  
FILING DATE: 13-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,379  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,382  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,730  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,021  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,022  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-21214/PL/CGC1911  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 397 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-478-14

Query Match 35.7%; Score 1052.5; DB 2; Length 397;  
Best Local Similarity 53.4%; Pred. No. 4e-99;  
Matches 212; Conservative 76; Mismatches 98; Indels 11; Gaps 3;  
QY 131 VLDYLYSGRVGDLAKAACLCVDEDCAHVGHCPAVAFMAQVLFPAASTFOVAELTNLFQRL 190  
Db 7 VLAYVYSSRVPPKGVSECADENCHVACRPVDFMLEVLYLAFIFKIPELITLYQRHL 66  
QY 191 LDVLDKVEVDNLLILSVANLCKSCMKLLERCLDMVYRSNLDMTITLESPLPPDVIKQII 250  
Db 67 LDVVDKVVIEDTLVILKLANICGKACMKLLDRCKEIIIVKSNVDVMSLEKSLPEELVKEII 126  
QY 251 DARLSGLISPENKGFPPKRVHRIHRALDSDDELVRMLLTGEGTNLDDAFALHYAVEHC 310  
Db 127 DRKELGLEVPVKV----KHVSNVHKALDSDDELVRMLLTGEGTNLDDAFALHYAVEHC 182  
QY 311 DSKITTELDLADLVNHRNPGYTVLHIAARRPKIIVSLTGTGARPADVTDFGRKAV 370  
Db 183 NVKATDLDLADLVNHRNPGYTVLHIAARRPKIIVSLTGTGARPADVTDFGRKAV 242  
QY 371 QISKRLTKGQDYGVEEGKPSKDLCEILEQAEERDPQGEASVSLAMAGESLGRGL 430  
Db 243 MIAKQATMAVECNIPQCKHSLKGLRCVLEIQEDKEQIPRDVPPSPFAVADELKMTL 302  
QY 431 LYLENRVALARIMFPMEARVAMDIQVDTGLEFNIGSGANPPPER----QRTVDLNEP 486  
Db 303 LDLENRVALAQRLEPTEAQAAMEIAEMKGTCEFIVTS---LEPDRLTGTGRTSPGVKIAP 359  
QY 487 FIMKEEHLARMTALSKTVELGKRFPPRCNSVLDKIMD 523  
Db 360 FRILEEHQSRKALKSKTVELGKRFPPRCNSAVLDQIMN 396

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RESULT 11
US-08-996-685-14
; Sequence 14, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Rvals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molins, Antonio
; APPLICANT: Ruess, Wilhelm
; APPLICANT: Knauf-Beiter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543
; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meligs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/PI/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-996-685-14
Query Match 35.7%; Score 1052.5; DB 3; Length 397;
Best Local Similarity 53.4%; Pred. No. 4e-99;
Matches 212; Conservative 76; Mismatches 98; Indels 11; Gaps 3;
QY 131 VLDYLYSGRVGDLPAACLCVDECAHVGHCHPAVAFNAQVLAFAASTFQVAELTNLFORRL 190
Db 7 VLAYVYSSRVPPPKGVSECADENCCHVACRPADVFMLEVLYLAFIPKIPILITLYORHL 66
QY 191 LDVLDKVEVDNLLILSVANLCKNSCKMLERCIDMVVRNLDMMITLEKSLPPDVIRKII 250
Db 67 LDVVDKVVIEDTLVILKLANICGKACMKLLDRCKEIIIVKSNVDMVSEKSLPEELVKEII 126
QY 251 DARLSGLISPENKGFNKHVRIHRAALSDDDVELVRLMTEGOTNDDAFALHYAVEHC 310
Db 127 DRKELGLEVPVKV---KHVSNNVHKALSDDIELVKLLKEDHTNDDACALHFAVAYC 182
QY 311 DSKITTELLDALADVNHNRPRGYTVLHIAARRRPEKIIIVSLTKGARPADVTDFGRKAV 370
Db 183 NVKATDLDLLADVNHNRPRGYTVLHVAAMRKEPOLILSLLEKGSASEATLEGRAL 242
QY 371 QISKRLTKOGDYEGVTEEGKPSKDRLCIELEQAEORRDPQLGEASVSLAMAGESLGRRL 430
Db 243 MIAQATMAVECNIPQCKHSLKGLCVLEIQEDRQEIIPRDVPPSFAVADELKWTLL 302
QY 431 LYLENRVALARIMFPMPEARVAMDAIQVDGTLEFNILGSGANPPPP---QRTTVDLNESP 486
Db 303 LDLENRVALAQLFPTEAQAAAMEIAEMKGTCEFTVTS---LEPDRLTGTRKTSFGVKIAP 359
QY 487 FIMKEEHLARMTALSKTVELGKRFPPRCNSVLDKIMD 523
Db 360 FRILEEHQSRKALSKTVELGKRFPPRCNSAVLDQIMN 396
RESULT 12
US-08-989-478-16
; Sequence 16, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382

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ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/996,685  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/761,543  
FILING DATE: 6-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,378  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,379  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,382  
FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,730  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,021  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,022  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,024  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/875,015  
FILING DATE: 16-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-996-685-16

FILING DATE: 27-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,730  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,021  
FILING DATE: 10-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/035,022  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 16:  
LENGTH: 261 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-478-16

Query Match 25.4%; Score 751; DB 2; Length 261;  
Best Local Similarity 54.6%; Pred. No. 1.3e-68;  
Matches 142; Conservative 54; Mismatches 56; Indels 8; Gaps 2;

QY 107 RLERLGEGGEEVEGYEARLRLVLDYLSRGVGLPKAACLCVDEDCAHVGHCPAVAF 166  
Db 10 KLEKEI----AKDYEGFDSVTVLAYVYSSRPPKGVSECADENCCHVACRPVDF 65

QY 167 MAQVLFPAASTFOVAELTNLFORRLDVLQKVEVDNLLILSVANLCNKSCKMLLERCLDM 226  
Db 66 MLEVLYLAFIKIPILTYLQRLHLDVVDKVIETDLVKLANICGKACMKLLDRCKEI 125

QY 227 VVRSNLDMTLEKSLPPDVIKQIDARLSGLISPEKNGFPNKHVRRIRHALDSDDELV 286  
Db 126 IVKSNVDMSLEKSLPEELVKEIIDRRKELGLEVPVKV----KHVSNVHKALDSDDELV 181

QY 287 RMLLTGQTNLLDFAALHVAHVECHDSKITTELLDLALADVNHNPRGYTVLHIAARRRP 346  
Db 182 KLLKEDHTNLDACALHFAVAYCNVKTATDLKLLDLADVNHNPRGYTVLHVAAMRKEP 241

QY 347 KIIVSLTKCARPDVTFDG 366  
Db 242 QLISLLEKASASEATLEG 261

RESULT 13  
US-08-996-685-16  
Sequence 16, Application US/08996685  
Patent No. 6031153  
GENERAL INFORMATION:  
APPLICANT: Ryals, John  
APPLICANT: Friedrich, Leslie  
APPLICANT: Uknes, Scott  
APPLICANT: Molina, Antonio  
APPLICANT: Ruess, Wilhelm  
APPLICANT: Knauf-Beiter, Gertrude  
APPLICANT: Kung, Ruth  
APPLICANT: Kessmann, Helmut  
APPLICANT: Oostendorp, Michael  
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6031153artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NO. 6031153th Carolina  
COUNTRY: USA

Query Match 25.4%; Score 751; DB 3; Length 261;  
Best Local Similarity 54.6%; Pred. No. 1.3e-68;  
Matches 142; Conservative 54; Mismatches 56; Indels 8; Gaps 2;

QY 107 RLERLGEGGEEVEGYEARLRLVLDYLSRGVGLPKAACLCVDEDCAHVGHCPAVAF 166  
Db 10 KLEKEI----AKDYEGFDSVTVLAYVYSSRPPKGVSECADENCCHVACRPVDF 65

QY 167 MAQVLFPAASTFOVAELTNLFORRLDVLQKVEVDNLLILSVANLCNKSCKMLLERCLDM 226  
Db 66 MLEVLYLAFIKIPILTYLQRLHLDVVDKVIETDLVKLANICGKACMKLLDRCKEI 125

QY 227 VVRSNLDMTLEKSLPPDVIKQIDARLSGLISPEKNGFPNKHVRRIRHALDSDDELV 286  
Db 126 IVKSNVDMSLEKSLPEELVKEIIDRRKELGLEVPVKV----KHVSNVHKALDSDDELV 181

QY 287 RMLLTGQTNLLDFAALHVAHVECHDSKITTELLDLALADVNHNPRGYTVLHIAARRRP 346  
Db 182 KLLKEDHTNLDACALHFAVAYCNVKTATDLKLLDLADVNHNPRGYTVLHVAAMRKEP 241

QY 347 KIIVSLTKGAPADYFDG 366  
Db 242 QLILSLERKASASEATLEG 261

RESULT 14

US-09-082-059-2  
; Sequence 2, Application US/09082059A  
; Patent No. 6225086  
; GENERAL INFORMATION:  
; APPLICANT: Morrow, Jon S.  
; TITLE OF INVENTION: No. 6225086el Ankyrin Proteins and a Method for Their Identification  
; FILE REFERENCE: 44574-5002-US  
; CURRENT APPLICATION NUMBER: US/09/082,059A  
; CURRENT FILING DATE: 1998-05-21  
; EARLIER APPLICATION NUMBER: 60/047356  
; EARLIER FILING DATE: 1997-05-21  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1088  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-082-059-2

Query Match 4.5%; Score 133; DB 4; Length 1088;  
Best Local Similarity 24.6%; Pred. No. 0.00021;  
Matches 66; Conservative 43; Mismatches 107; Indels 52; Gaps 12;

QY 254 LSLGLISPENKGPKNH-VRRIRHALSDDDVELVRMLLTEG-----QTNLDDAFALHYAV 307  
Db 301 VSLLRGNANVNSKSGTPLHLAQEDRVNVAEVLVNGQAHVDAQTKMGYT-PLHVGC 359  
QY 308 EHCDSKITTELLDALADVNNRPNRGYTVLHIAARREPKIIVSLTKGAPADYFDGR 367  
Db 360 HYGNIKIVNELLQHS-AKYNNAKTNGYTPHQAAQOGHTHIINVLQNNASPNELIVNGN 418  
QY 368 KAVQISKRLTKQGDYGVTEEGSPSKDRL-CIEILEQARRDPQLGEASVSL-----419  
Db 419 TALGIARRL-----GYISVVDTLKIVTEETMTTTEKHKMNVPTMNEVLDMSDDGED 474  
QY 420 AMAGESLGRLLYLENVALARIMFPEAR-VAMDIAQVDGTLFENLGSAGNPPPERQRT 478  
Db 475 AMTGDT-----DKYLGPDDLUKGLGDDSLPAEGYMGFSL--GARSASDRSYT 518  
QY 479 TVDLNESPFI-----MKEEHL 494  
Db 519 ---LNRSSYARDSMITEELLVPSKEQHL 543

RESULT 15

US-09-172-977-4  
; Sequence 4, Application US/09172977  
; Patent No. 5989863  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Yue, Henry  
; TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN  
; FILE REFERENCE: PF-0615 US  
; CURRENT APPLICATION NUMBER: US/09/172,977  
; CURRENT FILING DATE: 1998-10-14  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ ID NO 4  
; LENGTH: 1839  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: g29491

US-09-172-977-4

Query Match 4.3%; Score 127; DB 2; Length 1839;  
Best Local Similarity 21.1%; Pred. No. 0.002;  
Matches 81; Conservative 44; Mismatches 130; Indels 128; Gaps 14;

QY 69 GDLRVHRCVLSARSPPFLRGVFARRAAAAAGGGGEGDSERLELELLGGGEEVEVGEAL 128  
Db 475 GQVEVYRCLL-----RNGALVDARAREEQTPLHIASRLG-----KTEIV 513  
QY 129 RLVLVDYL-----YSGRVGDLPKAACLCVDEDCAH-----VGCHPAVA 165  
Db 514 QLLQLQWHPDAATTNGYTPLHISAREGQVDVASVL-LEAGAAHSLATKKGFTPLHVAAK 572  
QY 166 FMAQVLFPAASTFOVAELTNLFORRLDVLVDKVEVDNLLLSVANLCNCKMCLLERCLD 225  
Db 573 Y-----GSLDVAKL--LLQRRRA--AADSAGKNGLTPLHVAHYDNQKVALLL-----615  
QY 226 MMYRSNLDMITLEKSLPPDVI-----KQIIDARLSLGLISPENKGPKNK 269  
Db 616 -----LEKGASPHATAKNGYTPLHIAAKKNQMQIASTLLNYG---AETNIVTKQ 661  
QY 270 HVRIIRHALSDDDVELVRMLLTEG-----QTNLDDAFALHYAVE 308  
Db 662 GVTPLHLASQEGHTDMVTLLLDKGANIHMSTKSGLTSLHLAQEDRVNVAIDILTKHGADQ 721  
QY 309 HCDSKI-----TTELLDLAL---ADVNNRPNRGYTVLHIAARREPKIIVSL 353  
Db 722 DAHTKLGYTPLIIVACHYGNVKNVFNLLKQGANVNAKTNGYTPHQAAQOGHTHIINVL 781  
QY 354 TKGAPADYFDGRKAVQISKRL 376  
Db 782 QHGAKPNATTANGNTALAIKRL 804

Search completed: July 12, 2001, 17:13:02  
Job time: 24 sec

THIS PAGE OF 4NK (USPTO)



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2001, 17:12:39 ; Search time 13.17 seconds  
(without alignments)  
1513.796 Million cell updates/sec

Title: US-09-294-539-4  
Perfect score: 2952  
Sequence: 1 MEPTSHVTNAFSDSASV.....RSLSSSSSTSGAIRPRR 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Description
1	131	4.4	P16157 homo sapien
2	127	4.3	Q01484 homo sapien
3	123	4.2	P98150 gallus gall
4	123	4.2	Q02357 mus musculus
5	120.5	4.1	Q04861 gallus gall
6	119	4.0	P02566 caenorhabdi
7	116.5	3.9	Q06527 chromatium
8	116.5	3.9	Q05753 arabidopsis
9	116	3.9	Q46363 synchocyst
10	113.5	3.8	Q01630 caenorhabdi
11	112	3.8	P57078 homo sapien
12	111.5	3.8	Q15653 homo sapien
13	111.5	3.8	P47810 mus musculus
14	111.5	3.8	P25799 mus musculus
15	111	3.8	P21562 haloferrax s
16	111	3.8	P44838 haemophilus
17	110	3.7	Q16181 homo sapien
18	109	3.7	Q9wvc0 rattus norv
19	108	3.7	P19838 homo sapien
20	107.5	3.6	P31695 mus musculus
21	107	3.6	Q29346 archaeoglob
22	107	3.6	P28858 equine help
23	106.5	3.6	Q01705 mus musculus
24	106	3.6	P25963 homo sapien
25	106	3.6	Q63369 rattus norv
26	105	3.6	Q55131 mus musculus
27	105	3.6	Q99728 homo sapien
28	105	3.6	P96920 mycobacteri
29	105	3.6	P55203 bos taurus
30	104.5	3.5	P08566 s pentafunc
31	103.5	3.5	P34651 caenorhabdi
32	103	3.5	P45554 staphylococ
33	102.5	3.5	P30662 pseudorabid

34	102.5	3.5	849	1	TGR3_HUMAN	Q03167 homo sapien
35	102.5	3.5	898	1	KBF2_HUMAN	Q00653 homo sapien
36	102	3.5	256	1	SWH1_YEAST	P39555 saccharomyc
37	102	3.5	928	1	KINH_NEUCR	P48467 neurospora
38	102	3.5	1220	1	SLN1_YEAST	P39928 saccharomyc
39	102	3.5	1603	1	PSC_DROME	P35820 drosophila
40	101.5	3.4	752	1	PA26_MOUSE	P97819 mus musculus
41	101	3.4	492	1	FLIC_SALRU	P06175 salmonella
42	101	3.4	1108	1	DBS_HUMAN	O15068 homo sapien
43	100.5	3.4	866	1	RECE_ECOLI	P15032 escherichia
44	99.5	3.4	642	1	DNAK_FRATU	P48205 franciseila
45	99.5	3.4	2318	1	NTC3_MOUSE	Q61982 mus musculus

## ALIGNMENTS

RESULT 1  
ID ANK1\_HUMAN STANDARD; PRT; 1880 AA.  
AC P16157;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).  
GN ANK1 OR ANK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.  
RC TISSUE=Hematopoietic;  
RX MEDLINE=90158830; PubMed=2137557;  
RA Lux S.E., John K.M., Bennett V.;  
RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated  
RT structure with homology to tissue-differentiation and cell-cycle  
RT control proteins.";  
RL Nature 344:36-42(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90175370; PubMed=1698849;  
RA Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,  
RA Cheung M.C., Kan Y.W., Palek J.;  
RT "cDNA sequence for human erythrocyte ankyrin.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).  
RN [3]  
RP VARIANT HS ILE-462.  
RX MEDLINE=96225450; PubMed=8640229;  
RA Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,  
RA Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,  
RA Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;  
RT "Ankyrin-1 mutations are a major cause of dominant and recessive  
RT hereditary spherocytosis.";  
RL Nat. Genet. 13:214-218(1996).  
CC -!- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL  
CC ELEMENTS: BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO  
CC NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE  
CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.  
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE  
CC CYTOSOLIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;  
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.  
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC  
CC PLASMA MEMBRANE.  
CC -!- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY  
CC ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN  
CC VARIANT 2.1.  
CC -!- PTM: ACYLATED BY PALMITIC ACID GROUP(S).  
CC -!- PTM: ACYLATED BY PALMITIC ACID GROUP(S).  
CC -!- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE  
CC HEREDITARY SPHEROCYTOSIS (HS).  
CC -!- SIMILARITY: CONTAINS 23 ANK REPEATS.

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CC EMBL; X16609; CAA34610.1; -;  
CC EMBL; M28880; AAA51732.1; -;  
CC PIR; S08275; SJHUK.  
CC PIR; A35049; A35049.  
CC HSP; Q00420; IAWC.  
CC MIM; I82900; -;  
CC InterPro; IPR000488; -;  
CC InterPro; IPR000906; -;  
CC InterPro; IPR002110; -;  
CC Pfam; PF00791; ZU5; 1.  
CC Pfam; PF00023; ank; 22.  
CC Pfam; PF00531; death; 1.  
CC PROSITE; PS50088; ANK\_REPEAT; 20.  
CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
CC PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;  
KW Phosphorylation; Lipoprotein; Multigene family; Disease mutation;  
KW Elliptocytosis; Polymorphism.  
FT INIT\_MET 0  
FT DOMAIN 1 826  
FT 89 KDA DOMAIN (ANION EXCHANGE PROTEIN  
FT BINDING DOMAIN).  
FT 62 KDA DOMAIN (SPECTRIN BINDING  
FT DOMAIN).  
FT 55 KDA REGULATORY DOMAIN (REGULATES  
FT THE BINDING OF ANKYRIN TO SPECTRIN  
FT AND THE BAND 3 PROTEIN).  
FT 43 72  
FT REPEAT 76 105  
FT REPEAT 109 138  
FT REPEAT 142 171  
FT REPEAT 173 200  
FT REPEAT 204 233  
FT REPEAT 237 266  
FT REPEAT 270 299  
FT REPEAT 303 332  
FT REPEAT 336 365  
FT REPEAT 369 398  
FT REPEAT 402 431  
FT REPEAT 435 464  
FT REPEAT 468 497  
FT REPEAT 501 530  
FT REPEAT 534 563  
FT REPEAT 567 596  
FT REPEAT 600 629  
FT REPEAT 633 662  
FT REPEAT 666 695  
FT REPEAT 699 728  
FT REPEAT 732 761  
FT REPEAT 765 794  
FT DEATH DOMAIN.  
FT MISSING (IN ISOFORM 2.2).  
FT H->D (IN ISOFORM 2.2).  
FT TVEGPLEDPSELEVIDIDYMKSHKSTHTSTPNP -> ELRGS  
FT GLQPLIEGRKAQIVKRAKLRGKO (IN A THIRD  
FT ISOFORM).  
FT R->T.  
FT /FTId=VAR\_000595.  
FT V->I (IN HS).  
FT /FTId=VAR\_000596.  
FT R->H (IN BRUEGGEN).  
FT /FTId=VAR\_000597.  
FT V->A.  
FT /FTId=VAR\_000598.  
FT D->E.  
FT /FTId=VAR\_000599.  
FT

FT VARIANT 1391 1391 S -> T.  
FT /FTId=VAR\_000600.  
FT E -> D.  
FT /FTId=VAR\_000601.  
FT D -> N (IN DUESSELDORF).  
FT /FTId=VAR\_000602.  
FT R -> D.  
FT /FTId=VAR\_000603.  
FT CONFLICT 229 229 A -> S (IN REF. 2).  
FT CONFLICT 1545 1545 V -> I (IN REF. 2).  
SQ SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFDICD428 CRC64;  
  
Query Match 4.4%; Score 131; DB 1; Length 1880;  
Best Local Similarity 23.6%; Pred. No. 0.86;  
Matches 75; Conservative 34; Mismatches 103; Indels 106; Gaps 12;  
  
QY 271 VRRIRALSDDDVELVRLMLT-----EGQTNLDDAF----- 301  
Db 635 VTPHLAAQEGHAEMVALLLSKQANGNLKSGLTPLHLVAQEGHPVADVLIKHGVMVD 694  
QY 302 -----ALHYAVEHCDSKITTELLDALADYNHRNPRGYTVLHIAARREPKIIVSL 353  
Db 695 ATTRMGVTPLEHSHYGNIKLVKFLQ-HQADVNAKTGLGYSPLHQAQOGHTDIYTL 753  
QY 354 TKGARPADVTDFGRKAVQISKRLTKQDYFGVTEEGK-----PSPKDLRCI----- 399  
Db 754 KNGASPNVSDGTYTPLAIARL---GYISVTDVLKVVTDTSFVLVSKHRMSPETV 809  
QY 400 -EILEQAEERDPQLGEASVSLAMAGESLGRLLYLENRVALARIMFPPEARVAMIDIAQVD 458  
Db 810 DEILDVSEDE-----GEEL-----ISFKAERDSRDVDEEK 840  
QY 459 GTLEFNLGSGANPPRQRTTVDLNSPFTMKBEHLARMTALSKTVLGRFFPRCSNVL 518  
Db 841 ELLDF-----VPKLDQVV-----ESPAIPRI-----CAMPETVIRSEEQEQASKEY 883  
QY 519 DKIMDDETPVSLGRDYS 536  
Db 884 D---EDSLIPSPATETS 898  
  
RESULT 2  
ANK2\_HUMAN  
ID ANK2\_HUMAN STANDARD; PRT; 3924 AA.  
AC Q01484; Q01485;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).  
GN ANK2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain stem;  
RX MEDLINE=94075409; PubMed=8253844;  
RA Chan W., Kordeli E., Bennett V.;  
FT "440-kD ankyrinB: structure of the major developmentally regulated  
FT domain and selective localization in unmyelinated axons.";  
RL J. Cell Biol. 123:1463-1473(1993).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC TISSUE=Brain stem;  
RX MEDLINE=91302466; PubMed=1830053;  
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;  
FT "Isolation and characterization of cDNAs encoding human brain  
FT ankyrins reveal a family of alternatively spliced genes.";  
RL J. Cell Biol. 114:241-253(1991).  
RN [3]  
RP REVISIONS.

RA Carpentier S.;  
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 463-495 FROM N.A.  
 RX MEDLINE=92009921; PubMed=1833308;  
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,  
 RA Lux S.E., Ward D.C., Forget B.G.;  
 RT "Isolation and chromosomal localization of a novel nonerythroid  
 ankyrin gene";  
 RL Genomics 10:858-866(1991).  
 CC -!- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-  
 SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN  
 BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,  
 AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND  
 DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO  
 THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;  
 THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.  
 CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE  
 PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL  
 CELLS THROUGHOUT THE BRAIN.  
 CC -!- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES  
 AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE  
 AND FUNCTION (POTENTIAL).  
 CC -!- SIMILARITY: CONTAINS 23 ANK REPEATS.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))  
 DR EMBL; Z26634; CAB42644.1; -  
 DR EMBL; X56957; CAA40278.1; -  
 DR EMBL; X56958; CAA40279.2; -  
 DR EMBL; M37123; AAG62828.1; -  
 DR PIR; S14533; S14533.  
 DR PIR; A39643; A39643.  
 DR PIR; B39643; B39643.  
 DR PIR; S14569; S14569.  
 DR HSP; Q00420; IAWC.  
 DR MIM; 106410; -  
 DR InterPro; IPR000488; -  
 DR InterPro; IPR000906; -  
 DR InterPro; IPR002110; -  
 DR Pfam; PF00791; Z05; 1.  
 DR Pfam; PF00023; ank; 22.  
 DR Pfam; PF00531; death; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 20.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;  
 KW Phosphorylation; Multigene family.  
 FT REPEAT 63 92  
 FT REPEAT 96 125  
 FT REPEAT 129 158  
 FT REPEAT 162 191  
 FT REPEAT 193 220  
 FT REPEAT 232 261  
 FT REPEAT 265 294  
 FT REPEAT 298 327  
 FT REPEAT 331 360  
 FT REPEAT 364 393  
 FT REPEAT 397 426  
 FT REPEAT 430 459  
 FT REPEAT 463 492  
 FT REPEAT 496 525  
 FT REPEAT 529 558  
 FT REPEAT 562 591  
 FT REPEAT 595 624

FT REPEAT 628 657  
 FT REPEAT 661 690  
 FT REPEAT 694 723  
 FT REPEAT 727 756  
 FT REPEAT 760 789  
 FT REPEAT 793 822  
 FT DOMAIN 1773 1950  
 FT REPEAT 1773 1784  
 FT REPEAT 1785 1796  
 FT REPEAT 1797 1808  
 FT REPEAT 1809 1820  
 FT REPEAT 1821 1832  
 FT REPEAT 1833 1844  
 FT REPEAT 1845 1856  
 FT REPEAT 1857 1867  
 FT REPEAT 1868 1879  
 FT REPEAT 1880 1891  
 FT REPEAT 1892 1902  
 FT REPEAT 1903 1914  
 FT REPEAT 1915 1926  
 FT REPEAT 1927 1938  
 FT REPEAT 1939 1950  
 FT DOMAIN 3536 3620  
 FT VARSPLIC 1039 1039  
 FT VARSPLIC 1444 3528  
 FT CONFLICT 475 476  
 FT CONFLICT 971 971  
 FT CONFLICT 3581 3582  
 FT CONFLICT 3586 3586  
 FT SEQUENCE 3924 AA; 430337 MW; 52AC496C428E29D2 CRC64;  
 SQ  
 Query Match 4.3%; Score 127; DB 1; Length 3924;  
 Best Local Similarity 21.1%; Pred. NO. 4.2; Indels 128; Gaps 14;  
 Matches 81; Conservative 44; Mismatches 130;  
 QY 69 GDLRVHRCVLSARSFPLRGVFARRAAAAGGGGEGDSERLELRLGGGEEVGVYAL 128  
 DB 475 GQVEVYRCLL-----RNGALVDARAREEOTPLHIASRLG-----KTEIV 513  
 QY 129 RLVLVDYL-----YSGRVGLPKAACLCVDEDAH-----VGCHPAVA 165  
 DB 514 QLLQLQHMAHPDAATTNGYTPHISAREGQVDVASVL-LEAGAAHSLATKKGFTPLHVAAK 572  
 QY 166 FMAQVLFPAASTFOVAELTNLFQRLDLVDKVEVDNLLILSVANLCNCKMKLLERCLD 225  
 DB 573 Y-----GSLDVAKL--LLQRR--AADSAGKNGLTPLHVAAHYDNOKVALL----- 615  
 QY 226 MVVRSNLDMLTLEKSLPPDVI-----KOIIDARLSLGLISPENKGFPPN 269  
 DB 616 -----LEKGASPHATAKNGYTPHIAAKKNQMQIASTLLNVG---AETNIVTKQ 661  
 QY 270 HVRRIRHALDSDDDVLRMLLLEG-----QTNLDADAFALHYAVE 308  
 DB 662 GVTPLHLASQEGHTDMVTLLLDKGANHMTSKSLGTSLSHLAAQEDKVNVDILTCKGADQ 721  
 QY 309 HCDSKI-----TTELDLAL---ADVNHRNPRGYTVLHIAARREPKIIVSL 353  
 DB 722 DAHTKLGTYPLIVACHYGNVKNVFNLLKOGANVNAKTNGYTPHQAQOQHHTIINVL 781  
 QY 354 TKGARPADVTFCGRKAVQISKRL 376  
 DB 782 QHGAKPNATTANGTALAIKRL 804  
 RESULT 3  
 KBF2\_CHICK  
 ID KBF2\_CHICK STANDARD; PRT; 906 AA.  
 AC P98150;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT].

ANK 6.

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

GLY-RICH.

V -> G (IN REF. 2).

N -> F (IN REF. 2).

S -> K (IN REF. 2).

C -> G (IN REF. 2).

R -> SG (IN REF. 2).

R -> A (IN REF. 2).

E -> Q (IN REF. 2).

A -> G (IN REF. 2).

T -> A (IN REF. 2).

VRVP -> SEA (IN REF. 2).

L -> RC (IN REF. 2).

SPILLSPPPPSRNHL -> RPDTELTTPRAGNV (IN REF. 2).

T -> S (IN REF. 2).

Y -> D (IN REF. 2).

T -> D (IN REF. 2).

ASAL -> SVSL (IN REF. 2).

P -> A (IN REF. 2).

R -> A (IN REF. 2).

R -> A (IN REF. 2).

OE0CE20DB4F30E62 CRC64;

99667 MB;

4.2%; Score 123; DB 1; Length 906;

Best Local Similarity 19.7%; Pred. No. 1.1;

Matches 105; Conservative 59; Mismatches 199; Indels 170; Gaps 18;

QY 63 GGGGGGDLRVHRCVLSRSPFLRGVFAARRAAAAGGGE---DGSRLRELRELLGGGGE 119

DB 356 GGAGGAGGF-----GAGGGNLSFPYSGGLGYNLYSSPH 391

QY 120 EYEGYEAALRLVLYSGRVD---LPKAACLCVDECAHVCH----- 161

DB 392 PVGGYQG--GVQKKAASERDGDQAPTESTYCRELQRHRLHCLWLLARRNAHALDY 449

QY 162 -----PAVAFMAQVLFASFTQ-----VAELNLFQRLDLDKVEVDNLLIL 206

DB 450 SVTADPRMLLAVQRHLAASODENGDTPLHLAIHQETAVI-KQIEVVVSIPOQII--- 505

QY 207 SVANLCKNSCKMLERCIDMVVRNLDMLTLEKSLPDVVIKQIIDARLSGLISPENKGF 266

DB 506 ---NITNN-----LQOTPLHAVITKO--POVVQLLEAHANPTLLDRYNSL 548

QY 267 PNKHVRIRHRLDSDVVELVRL----- 290

DB 549 -----LHLALQAADEMLRLHLAHLASATPYLLHLPNFOGLLPVHLAVKAKSPACLDL 601

QY 291 -----TEGQNLDDAPALHYAVEHCDKITTETLDDALADVNRNRPGRYTVLHIAARR 343

DB 602 LVKRGADYNGVERGQGRTPPLHAVEMENLNATHLVKKGANVNSRTFAGNTPHLAAGL 661

QY 344 REPKIIVSLTKGAPADVTGGRKAVOISKRLLTKQGDYFGVTEGKPSKDRLCIELE 403

DB 662 GSPTLTKLLKAG---ADVQRENDEPVSPSSVRVPSSD-----TDGDE-----E 703

QY 404 QAERDPPOLGEASVSLAMAGESLGRLLYLENRVALARIMFPMEARVAMDAQVDTLEF 463

DB 704 QEQEAMELGEPALSPHTPEE-----EQEAGPR-----QRLHTALDITRSQKYRDI 751

QY 464 NLGSG-----ANPPPERQRTTVDLNEPSPFIMKEEHLARMTALSKTVELGKR 509

DB 752 LQASQSPPIILSCPPPSRNLHSLDLDALQGLQLLNQYSGSGDMWELAKR 804

RESULT 4

ANKL\_MOUSE

ID ANKL\_MOUSE STANDARD: PRT; 1862 AA.

AC Q02357;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)



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EMBL; M86930; AAA49000.1; -  
EMBL; D13719; BAA02872.1; -  
PTR; A41996; A41996.  
InterPro; IPR000451; -  
InterPro; IPR000488; -  
InterPro; IPR002110; -  
Pfam; PF00554; RHD; 1.  
Pfam; PF00023; ank; 6.  
Pfam; PF00531; death; 1.  
PRINTS; PR00057; NFKBTNSCPCT.  
PROSITE; PS50088; ANK\_REPEAT; 5.  
PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
PROSITE; PS01204; REL\_1; 1.  
PROSITE; PS0254; REL\_2; 1.  
DNA-binding; Transcription regulation; Activator; Nuclear protein;  
phosphorylation; Repeat; ANK repeat.  
DOMAIN 47 372  
REL-LIKE (RHD).  
REPEAT 540 569  
REPEAT 579 608  
REPEAT 612 641  
REPEAT 648 677  
REPEAT 682 712  
REPEAT 716 745  
REPEAT 769 799  
DOMAIN 365 370  
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
MOD\_RES 342 342  
CONFLICT 111 111  
CONFLICT 513 513  
CONFLICT 696 696  
CONFLICT 708 708  
CONFLICT 710 710  
CONFLICT 718 718  
CONFLICT 848 848  
CONFLICT 868 868  
CONFLICT 875 875  
CONFLICT 898 899  
CONFLICT 903 903  
CONFLICT 972 984  
SEQUENCE 984 AA; 108169 MW; A3B75AE6AF453FA4 CRC64;  
REF. 2).

Query Match 4.1%; Score 120.5; DB 1; Length 984;  
Best Local Similarity 22.4%; Pred. NO. 1.8;  
Matches 115; Conservative 67; Mismatches 212; Indels 119; Gaps 22;  
QY 137 SRGVGLDPAACLCVDE-DCAHVGCHPAVAFMAQVLFRASTFOVAE--LTNLFQ----- 187  
DB 470 SGHNEEKEDASLCCKDEGNKRCGQDG-----LFLEKAMQLAKRHCNRLFVAVTGD 522  
QY 188 -RLLDV---LDKVEVDN---LLILSVANICNCKMILLERCLDMVRSNLDN----- 234  
DB 523 VRMLLAQVRLTAQDNGDNVHLISIIHLHRELKVNLEVPDNNYINRNDLYQT 582  
QY 235 -----ITLEKSLPDVVK-----QIADAR-----LSGLISPENK--GFPNKH----- 270  
DB 583 PLHLAVITKQAEVVEELLKAGANVLLDRHGSVHLAAAGDDKILSLLLKHQKASSMI 642  
QY 271 -----VRIIRALSDSDVELVRLMLTTEG-----QTNLDDAFALHYAVEHCDSKITTEL 318  
DB 643 DLNSGEGLSAIHVVVTANSLSCLKLLIAAGVDVNAQEQSKSGRTALHLAVEQENVPLAGCL 702  
QY 319 LDLALADVNRHPRGVTYVLIHIAARRRKKIIVSLITKGAAPADVTFDGRKAVQISKRLTK 378  
DB 703 LLEGADVSTYDGTTPHLHIAAGRGFTKLAVALKAAGADPHVENFE----- 749

QY 379 QGDYFGVTEGPKRDKR-----LCIEILEQAERDPOLGEASVSLAMAGESL--RGRL 430  
DB 750 --PLFVEEDVDKDDDDDEIGVPGTTPDAAANWEVDIINGRPYIAAAVSEDLISQGPL 807  
QY 431 LYLENVALARIMFPMEARVAMDIAQVDTGLEFNLSG-----ANPPPERQRTVVDLN 483  
DB 808 REL-NESSKOQLYKLE---TPDPSKNWSTLAELKGLILNNAFQLSPSP--SKTLDDNY 861  
QY 484 ESPFIMKEHLARMTALSKT-----VELGKRFPFRCNSVLDKIMD--DETDPVSLGRDVS 536  
DB 862 KISGGTGQELIAAFTQMDHTEAIEVIQKALSSQSRSHOEDKTIEAFPSLSPFAKET 921  
QY 537 AEKKRFRHDLQVLFQAFKAFKEDKEENDRSGLSSS 569  
DB 922 GE-----LYNHKFDPESTCDSGVETS 943  
RESULT 6  
MYSB\_CAEEL  
ID MYSB\_CAEEL STANDARD; PRT; 1966 AA.  
AC P02566;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE MYOSIN HEAVY CHAIN B (MHC B).  
GN UNC-54 OR MYO-4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83273600; PubMed=6576334;  
RA Karn J., Brenner S., Barnett L.;  
RT "Protein structural domains in the Caenorhabditis elegans unc-54  
myosin heavy chain gene are not separated by introns."  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).  
[2]  
RP SEQUENCE OF 850-1966 FROM N.A.  
RX MEDLINE=82272395; PubMed=7202124;  
RA McLachlan A.D., Karn J.;  
RT "Periodic charge distributions in the myosin rod amino acid sequence  
match cross-bridge spacings in muscle."  
RL Nature 299:226-231(1982).  
[3]  
RP SEQUENCE OF 1876-1966 FROM N.A.  
RX MEDLINE=83232892; PubMed=6571695;  
RA Wills N., Gesteland R.F., Karn J., Barnett L., Bolten S.,  
RA Waterston R.H.;  
RT "The genes sup-7 x and sup-5 III of C. elegans suppress amber  
nonsense mutations via altered transfer RNA."  
RL Cell 33:575-583(1983).  
CC -1- FUNCTION: MUSCLE CONTRACTION.  
CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2  
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC),  
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).  
CC -1- SUBCELLULAR LOCATION: THICK FILAMENTS OF THE MYOFIBRILS.  
CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING  
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,  
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.  
CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY  
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.  
CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT  
MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE  
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED  
SUBFRAGMENT (S2).  
CC -1- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C.  
ELEGANS.  
CC -1- MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE BODY  
WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.  
CC -1- SIMILARITY: THE GLOBULAR HEAD AA SEQUENCE SHOWS A HIGH DEGREE OF  
SIMILARITY WITH THE GLOBULAR HEAD SEQUENCES OF MUSCLE & NONMUSCLE  
HEAVY CHAINS. BY CONTRAST THE ROD SEQUENCE IS LESS CONSERVED, BUT

THE PERIODICITIES OF HYDROPHOBIC & CHARGED RESIDUES, WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE, ARE CONSERVED.

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EMBL: J01050; AAA28124.1; -  
EMBL: V01494; CAA24738.1; -  
PIR: A02992; MKWK  
HSP: P08799; 1MND  
InterPro: IPR001609; -  
InterPro: IPR002928; -  
Pfam: PF01576; Myosin\_tail; 1.  
Pfam: PF00063; myosin\_head; 1.  
PRINTS: PR00193; MYOSINHEAVY.  
KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;  
KW ATP-binding; Methylation; Alkylation; Heptad repeat pattern;  
KW Multigene family.  
FT DOMAIN 1 850 GLOBULAR HEAD (S1).  
FT DOMAIN 851 1966 RODLIKE TAIL (S2 AND LMM DOMAINS).  
FT DOMAIN 851 1164 ALPHA-HELICAL TAILPIECE (S2).  
FT DOMAIN 1165 1966 LIGHT MEROMYOSIN (LMM).  
FT DOMAIN 851 1966 COILED COIL (POTENTIAL).  
FT NP\_BIND 177 184 ATP (BY SIMILARITY).  
FT DOMAIN 665 687 ACTIN-BINDING.  
FT DOMAIN 769 783 ACTIN-BINDING.  
FT MOD\_RES 128 128 METHYLATION (TRI-) (POTENTIAL).  
FT MOD\_RES 705 705 ALKYLATION (SH-1).  
FT MOD\_RES 715 715 ALKYLATION (SH-2).  
FT DOMAIN 1165 1176 HINGE.  
FT CONFLICT 1337 1337 E -> R (IN REF. 2).  
FT CONFLICT 1880 1880 I -> L (IN REF. 2).  
FT SEQUENCE 1966 AA; 225125 MW; B66F0BB2FE27B67F CRC64;

Query Match  
Best Local Similarity 4.0%; Score 119; DB 1; Length 1966;  
Matches 129; Conservative 106; Mismatches 226; Indels 190; Gaps 32;

QY 13 SDSASVVE-----GDA-DADADVE-----AL-----RLSDNLAA 44  
DB 1419 ANSKNASLEKTSRLVGLDDDDAQVDVERANGVASALEKQKQFKDIIDEWKRKTDLLAAE 1478  
QY 45 FRSPEDFAFLADARIAVPGGGGGGDLRVHRCVLSARSPLRGVFARR-----AAAAAGGGE 102  
DB 1479 L-----DGAQRDLR-----NTSTDLFKAKNAQEELAEVVEGLRRE 1513  
QY 103 DGSERLELREL---LGGGGEV-----EVGYEARLRVLVDLYSRVGDLPRAACL 149  
DB 1514 NKSLSOEIKDLTDLGEGGRSVHEMOKIIRLEIEKEELQHAL-----1556  
QY 150 CVDECAHVGCCHPAPAFMAQVLFAASTFOVAELTNLFORLLDVLDKVEVDNLLILSYA 209  
DB 1557 --DEAAALEAESKVLRAQV-----EVSQRSIEKRIQE--KEEFEN-----T 1598  
QY 210 NLNCKSMKLLERCLDMVYRSLNMDITLESPPDVIKQIIDARISLGLISPENKGFNNK 269  
DB 1599 RKNHRALESQASLETEAKGRAELRIKKLEGD-----INELEIALDHANKANAD-AOK 1653  
QY 270 HVYRIHRLDSDDELVELVRLMFTGGTNLDLDAFALHYAVHEHCDSKITTELLDLALAD---V 326  
DB 1654 NLKRY-----QEQVRELQVQVEEQNGADTREQFENAEKRALTLQSEKELLVANAEEA 1708  
QY 327 NHRNPRGYTVLHIAARRRREPKEIIVSLITKGPADVTDFGRKAVQISKRLTKQDFFGYT 386  
DB 1709 RARKQAEYEAADARDQANANAAQVSSLSAKRKLGEIQAIHA-DLDETL---NEYKAAE 1764  
QY 387 EEGKPSPKD--RLCIEILQAEARR-----DPOLGEASVSLAMA-GESLRGLLYL 433

DB 1765 ERSKKAIAATRLAEELRQEHSHQVDRLRKLEQLKLEIQVRLDEAAALKGG-----1820  
QY 434 ENRVALARIMFMEARVAMDIQAQVDTGLBFLNLGSGANPPPERQRTTVDLNESEPFIMKEEH 493  
DB 1821 -----KKVIAKLEQRVRELSLDG-----EQRREFODANKN--LGRADR 1857  
QY 494 LARMTALSKTVELGKRFPPRCNSNVLDKIMD-----DETDPVSLGRDTSNEKERRF- 543  
DB 1858 --RVRELQFQVDEDKNFERLQDLIDKLOOKLTKQKKVQEEAEELA---NLNLQYKQULT 1912  
QY 544 HDLQVQLQKAFHEDKEENDRSGLSSSS-----SSTSICAIR-PRR 582  
DB 1913 HQLEDAEERA---DQAEUSLSKMRSKSRASASVAPGLQSSASAASVIRSPSR 1960

RESULT 7  
ANKH\_CHRVI  
ID ANKH\_CHRVI STANDARD; PRT; 323 AA.  
AC Q06527;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE ANKYRIN HOMOLOG PRECURSOR.  
OS Chromatium vinosum.  
OC Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;  
OC Allochromatium.  
OX NCBI\_TaxID=1049;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D / ATCC 17899 / DSM 180;  
RX MEDLINE=93300842; PubMed=8390993;  
RA Dolata M.M., van Beeumen J.J., Ambler R.P., Meyer T.E.,  
RA Cusanovich M.A.;  
RT "Nucleotide sequence of the heme subunit of flavocytochrome c from  
RT the purple phototrophic bacterium, Chromatium vinosum. A 2.6-kilobase  
RT pair DNA fragment contains two multiheme cytochromes, a flavoprotein,  
RT and a homolog of human ankyrin."  
RL J. Biol. Chem. 268:14426-14431(1993).  
CC -!- SIMILARITY: CONTAINS 8 ANK REPEATS.  
CC -----  
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EMBL: L13419; AAA23315.1; -  
DR HSP: Q00420; 1AMC  
DR InterPro: IPR002110; -  
DR Pfam: PF00023; ank; 8.  
DR PROSITE; PS00088; ANK\_REPEAT; 7.  
DR PROSITE; PS0297; ANK\_REPEAT\_REGION; 1.  
KW Signal; ANK repeat; Repeat.  
FT SIGNAL 1 28 POTENTIAL.  
FT CHAIN 29 323 ANKYRIN HOMOLOG.  
FT REPEAT 31 60 ANK 1.  
FT REPEAT 64 93 ANK 2.  
FT REPEAT 97 126 ANK 3.  
FT REPEAT 130 159 ANK 4.  
FT REPEAT 163 192 ANK 5.  
FT REPEAT 196 225 ANK 6.  
FT REPEAT 229 258 ANK 7.  
FT REPEAT 262 291 ANK 8.  
SQ SEQUENCE 323 AA; 33453 MW; 3976D34A9BD607DF CRC64;

Query Match  
Best Local Similarity 3.9%; Score 116.5; DB-1; Length 323;  
Matches 72; Conservative 31; Mismatches 108; Indels 49; Gaps 9;

QY 277 ALDSDVVELVRLMLTEG-----QTNLDDAFALHVAVEHCDSKITTELDLALADVNHRNPR 332  
 Db 72 AVEGDDETVALLSRGADVNARTVACCTPLTFAAEAGHIGISALLERG-AHVHDETRS 130  
 QY 333 GYTVLHIAARRRPEKIIISLLTKGAPADVTFGKRAVQISKRLTKGQDGYFGVTEGKPS 392  
 Db 131 GWDALMTASRHGIDTMDVEQLLFGKADPAADREGRTALM---QAASKGE-TGVLP-----181  
 QY 393 PKDRLCTEILEQAEERDPO-----LGEASVSLAMAGESLRGLLYLENRRVAL---ARIMEF 444  
 Db 182 ----LLIEGGADLEARDQKQATALLIAAQOQAGAVETLAGLGAQLDQAVDALGSTALILA 237  
 QY 445 PMEARVAMIDIAQVDCGLEFNLSGANPPPERQRTVDLINESPFIMKEHLARM-----497  
 Db 238 VGHGHVAM-----VERLLAMGADPNRQDKCTTALMEAVATDHAELIDRLIAAGART 289  
 QY 498 -----TALSKTVELGKR 509  
 Db 290 DLKDDADRTAADIADVQLGHR 309

## RESULT 8

AKR\_ARATH  
 ID AKR\_ARATH STANDARD; PRT; 439 AA.  
 AC Q05753;  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE ANKYRIN REPEAT PROTEIN (AKRP).  
 GN AKR.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=CV, C24; TISSUE=Leaf;  
 RX MEDLINE=93104681; PubMed=1281700;  
 RA Zhang H., Scheifer D.C., Fowle W.H., Goodman H.M.;  
 RT "Expression of chloroplast or sense RNA of an ankyrin repeat-containing  
 gene blocks chloroplast differentiation in Arabidopsis.";  
 RL Plant Cell 4:1575-1588(1992).  
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE TEMPORAL AND SPATIAL REGULATION  
 OF CHLOROPLAST DEVELOPMENT FROM PROPLASTID.  
 CC -1- DEVELOPMENTAL STAGE: HIGHEST EXPRESSION OCCURS IN TWO-WEEK-OLD  
 CC PLANTS AND DECLINES AS PLANTS DEVELOP FURTHER.  
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.

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DR EMBL; M82883; AAA32812.1;  
 DR PIR; JQ1729; JQ1729.  
 DR HSSP; Q13625; LYCS.  
 DR InterPro; IPR002110;  
 DR Pfam; PF00023; ank; 4.  
 DR PROSITE; PS00088; ANK\_REPEAT; 3.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 KW Cytoskeleton; Repeat; ANK repeat; Multigene family.  
 FT REPEAT 288 317 ANK 1.  
 FT REPEAT 321 350 ANK 2.  
 FT REPEAT 354 383 ANK 3.  
 FT REPEAT 387 416 ANK 4.  
 SQ SEQUENCE 439 AA; 49150 MW; C371A90028B25BF3 CRC64;

\*Query Match

3.9%; Score 116.5; DB 1; Length 439;

Best Local Similarity 28.5%; Pred. No. 1.1;  
 Matches 51; Conservative 26; Mismatches 63; Indels 39; Gaps 6;  
 QY 188 RRLDVLVDKEVDNLLILSVANLCKNSCKMLERC-----LDMVRSNLDMLTLEKSLP 242  
 Db 264 RKLLSKEEFMLNRPDPLAVATSKKWLPLHTLAACGEFYLDLSLKHLND-----314  
 QY 243 PDVIKQIIDARLSGLISPENKGFNKHVRRIHRALDSDDELVRMLLTGQTN--LDD- 299  
 Db 315 -----INATDVGGTLA-----LHRAIGKKQAITNVLNRESANPFVLDDE 354  
 QY 300 -AFALHVAVEHCDSKITTELDLALADVNHRNPGVTVLHIAARRRPEKIIISLLTKGA 357  
 Db 355 GATLMHVAVOTA-SAPTIKLLLYNADINADRDGTPLHVAQVARRSDIVKLLIKGA 412

## RESULT 9

ZAM\_SYNY3  
 ID ZAM\_SYNY3 STANDARD; PRT; 782 AA.  
 AC Q46363; P73254;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE ACETAZOLAMIDE CONFERRING RESISTANCE PROTEIN ZAM.  
 GN ZAM OR SLL1910.  
 OS Synecocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95244838; PubMed=7727754;  
 RA Beuf L., Bedu S., Cami B., Joset F.;  
 RT "A protein is involved in accessibility of the inhibitor  
 acetazolamide to the carbonic anhydrase(s) in the cyanobacterium  
 Synecocystis PCC 6803.";  
 RL Plant Mol. Biol. 27:779-788(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,  
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,  
 RA Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synecocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 CC -1- FUNCTION: NOT KNOWN; CONTROL RESISTANCE TO THE CARBONIC ANHYDRASE  
 CC INHIBITOR ACETAZOLAMIDE.  
 CC -1- SIMILARITY: BELONGS TO THE RIBONUCLEASE II (RNB) FAMILY.

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DR EMBL; X80179; CAA56462.1;  
 DR EMBL; D90904; BAAL7281.1;  
 DR InterPro; IPR001900;  
 DR InterPro; IPR003029;  
 DR Pfam; PF00773; RNB; 1.  
 DR Pfam; PF00575; SL; 1.  
 DR PROSITE; PS01175; RIBONUCLEASE\_II; 1.  
 DR Hydrolase; Exonuclease; Nuclease.  
 FT CONFLICT 59 59 N -> K (IN REF. 2).  
 FT CONFLICT 123 124 EQ -> G (IN REF. 2).  
 FT CONFLICT 246 250 TWITA -> ODIR (IN REF. 2).  
 FT CONFLICT 479 479 G -> A (IN REF. 2).  
 FT CONFLICT 490 490 G -> E (IN REF. 2).





[illegible]

QY 100 GGDGSGERLELRELIGGGEEVEVGEALRL-----VLDLYSGRVGDLPKAACLCV 151  
DB 79 GFSAGTEYMDLQN-----DLGQTAHLAAILGETSTVEKLYAAGAG-----LCV 122  
QY 152 DEDCAHVGHCPAVAFMAQVLAFASTFQVLAETNLNFORLLDVLVDKVEVDNLLILSVANL 211  
DB 123 AERRGHTALHACRGVACHACARA-----LLQPRPRPREAPD----- 159  
QY 212 CNKSKMKLLERCLDMVVRNLDMLTIL--EKSLLPPDVIKIIDLARLSGLISPEN-KGFPN 268  
DB 160 -----TYLAQGDPRTPDNTNHTFVALYPSDLEKEESEEDWKLOL-----EAEENYEGHTP 210  
QY 269 KHVRRHRLDSDVDELVRMLLTGEGTNLDAPALHVAVEHCDKSKITTELLDLALADVNH 328  
DB 211 LHVAVIHK-----DVEVRLLRDAG-----ADLDK 235  
QY 329 RNPGR-GYTVLHIAARREPKIIVSLTKGARPADVTDFGRKAV-----QISKRLTKQ 379  
DB 236 PEPTCGRSLPHLAVEAQAADVLELLLRAGANPAARMYGGRTPLGSAMLRPNPILARLLR- 294  
QY 380 GDYFEGYTECKPSKPKRLCIEILQAEERRDPQLGEASVS 418  
DB 295 -----AHGAPEP-----EGEDKSGPCSS 314

## RESULT 13

WEEL\_MOUSE STANDARD; PRT; 646 AA.  
AC P47810;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE WEEL-LIKE PROTEIN KINASE (EC 2.7.1.112).  
GN WEEL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Calvaria;  
RX MEDLINE=96028438; PubMed=7551544;  
RA Honda R., Tanaka H., Ohba Y., Yasuda H.;  
RT "Mouse p87weel kinase is regulated by M-phase specific  
RT phosphorylation."  
RL Chromosome Res. 3:300-308(1995).  
RN [2]  
RP BINDING TO PROTEIN 14-3-3 ZETA.  
RX MEDLINE=97168955; PubMed=9016762;  
RA Honda R., Ohba Y., Yasuda H.;  
RT "14-3-3 zeta protein binds to the carboxyl half of mouse weel  
RT kinase."  
RL Biochem. Biophys. Res. Commun. 230:262-265(1997).  
CC -!- FUNCTION: COULD ACT AS A NEGATIVE REGULATOR OF ENTRY INTO MITOSIS  
CC (G2 TO M TRANSITION). THIS KINASE SPECIFICALLY PHOSPHORYLATES  
CC CYCLIN B-DEPENDENT CDC2 EXCLUSIVELY ON TYR-15. BINDS TO 14-3-3  
CC PROTEIN ZETA.  
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
CC TYROSINE PHOSPHATE.  
CC -!- ENZYME REGULATION: NEGATIVELY REGULATED BY PHOSPHORYLATION IN  
CC THE M-PHASE.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).  
CC -!- PTM: PHOSPHORYLATION IS DUE TO AT LEAST 2 KINASES. CYCLIN-CDC2  
CC PHOSPHORYLATION, WHICH OCCURS THROUGHOUT THE CELL CYCLE, APPEARS  
CC NOT TO BE THE ONLY REGULATORY KINASE ACTIVITY. WEEL-LIKE KINASE  
CC IS ALSO AUTOPHOSPHORYLATED.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC WEEL SUBFAMILY.

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DR EMBL; D30743; BAA06404.1;  
DR MGI; MGI:103075; Weel.  
DR InterPro; IPR000719;  
DR InterPro; IPR002290;  
DR Pfam; PF00069; pkinase; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW Mitosis; Transferase; Tyrosine-protein kinase; ATP-binding;  
KW Phosphorylation.  
FT DOMAIN 34 42 POLY-GLU.  
FT DOMAIN 74 77 POLY-ARG.  
FT DOMAIN 97 101 POLY-GLY.  
FT DOMAIN 298 568 PROTEIN KINASE.  
FT NP\_BIND 304 312 ATP (BY SIMILARITY).  
FT BINDING 327 327 ATP (BY SIMILARITY).  
FT ACT\_SITE 425 425 BY SIMILARITY.  
FT MOD\_RES 123 123 PHOSPHORYLATION (BY CDC2) (POTENTIAL).  
FT MOD\_RES 139 139 PHOSPHORYLATION (BY CDC2) (POTENTIAL).  
SQ SEQUENCE 646 AA; 71664 MW; AD4144C913D277B8 CRC64;

Query Match 3.8%; Score 111.5; DB 1; Length 646;  
Best Local Similarity 18.2%; Pred. No. 4;  
Matches 135; Conservative 92; Mismatches 236; Indels 279; Gaps 30;  
QY 3 PPTSHVTNAPS-----DSDASVVEGDADADADVEALRLRLSDNLAAPRSP 49  
DB 10 PPTRVCAAYSLRQKLIFSPGDCDEEEEGEGHSTGEDSAFQEPDPLSA-RSPA 68  
QY 50 DFAFLADARITAVPG-----GGGGDLRVHRCVLSARSFPLRGVFARRAA 94  
DB 69 EAE--AQRRRSPGAPSPSGELEDLLQLGGGG-----A 102  
QY 95 AAAGGEGDGSERLELRELIGGGEEVEVGEALRLVLDLYS---GRVGDLPKAC-- 148  
DB 103 QAAGGAGDGSWE-----GFGSSPVKSPSTAYFLSSPFPVRCGGPGDASPGCGA 156  
QY 149 -LCVDEDCAHVGHCPAV---AFMAQVLF-----AASFQV 179  
DB 157 PRAMDDPCSPQDPYPTPPHKTFRKLRLFTPTPKSLLSKARVIDSGSVKLGSSLFMD 216  
QY 180 AELTNLFORLLDVLDKVEY-----DNLL----- 204  
DB 217 TEKSG--KREFDTRQTPQVNIPTDPVLLHSSGRCGRKRAYFNDSSEDEASDYEF 273  
QY 205 -----ILSVANLCNK-----SCMKLLERCLDMVVRNLD 234  
DB 274 EDETRPAKRITITENSKSRYYTFEFHELEKIGSGEFGSVFKVRLDGCYIAIKRS--- 329  
QY 235 ITLEKSLPPDVIKQ---IIDARLSGLISPENKGNPKHVRHRLDSDVDELVRMLL 290  
DB 330 ---KKPLAGSVDEQNALREVIYAHVIG-----OHPHVVRVFSAAEDHMLQNEY 377  
QY 291 TEGQTNLDALFALHYAVEHCDSKITTELLDLALADVNHNRNPRGYTVLHIAARREPKIIV 350  
DB 378 CNG-GSLADAISENY-----RVMSYLTEVELKDLLQLVGRGLYIH-----SM 419  
QY 351 SLTKGARPADVTDFGRKAVQ-----ISKRLTKQGDYFEGVTEEGKPSKDR- 396  
DB 420 SLVHMDIKFNSI-FISRTSIPNAVSEEGDEYDWNKVMFKIGDLGHDTRISSPQLEEGD 478  
QY 397 ---LCIEILLEQAEERRDPQLGEASVSAM---AG-----ESLGRGL-----LYL 433  
DB 479 SRELANEVQENYSHLPKADIFALATVVCAGAAELPRNGEHWHEIRQRLPRIPQVLS 538  
QY 434 ENRVALARIMFMEARVAMDIAQVDGTLFNLGSGANPPPERQRTTVDLINESPFINKEEH 493



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FT REPEAT 714 743 ANK 6.
FT REPEAT 767 797 ANK 7.
FT DOMAIN 358 363 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 335 335 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT VARSPLIC 780 971
FT
FT IDPKNNATLAQKLGILGLNNAFLRSLPAPSTLMDNVEVS
FT QTKELMALQOMGYTEAIEVIOAFTPTATSSPVTTA
FT GVHCLPLSSSRQHIDELSDSCVDSGVTSFRKLSPTE
FT SLTGDSPLLSLKNKPHGYQEGPIEGKI -> GT (IN
FT ISOFORM P84).
FT VARSPLIC 860 971 VSGGTIKELMALQOMGYTEAIEVIOAFTPTATSSPVTT
FT QTKELMALQOMGYTEAIEVIOAFTPTATSSPVTTA
FT TSGLACDPLSSSRQHIDELSDSCVDSGVTSFRKLSPTE
FT ASVTIVVRRHPSANSALQSLLETAHCYL (IN ISOFORM
FT P98).
SQ SEQUENCE 971 AA; 105641 MW; E03687260192A934 CRC64;

Query Match 3.8%; Score 111.5; DB 1; Length 971;
Best Local Similarity 20.4%; Pred. No. 6.9;
Matches 95; Conservative 61; Mismatches 159; Indels 151; Gaps 19;

QY 89 FARRAAAAGGGGDSERLELELRLGGGEEVEGYEALRLVLDLYSG-----138
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 372 FGGGSGAGAGGGGFGSG-----GGGGSTGSPG-----PGYGSYNGPPPYGGIT 416
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 139 -----RVGDLPKAACLCVDEDAHV-----GCHPAVAFWAQV 170
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 FHPGVTKSNAGVTHGTINTFKNGPKDKCAKSDDESLTPEKETEGEGSPLMACKTTEP 476
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 LFAASTFQVAELTNLQRRLLDVKVEVDNLLILSVANLCKNCKMKLLER-----CLDM 226
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 477 IALASTWEKQDMQFQ-----DNLEL-----EKALQLARRHANALFDY 515
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 227 VRSNLDMTLEKSLPPDVIKIIDARLSGLISPENKGFPPKHKVRIIRALDSDVELV 286
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 516 AVTGDVKKLLAVQRLHATVQDENGSLVHLAI-----HLHAQLVRDLLEVT 562
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 287 RMLLTGQTNL--DAF--ALHYAVEHCDSKITTELDLALADVNHRNPRGYTVLHIAARR 343
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 563 SGLISDIIINMRNDLYOTPLHLAVITKQEDVVEDLLRVG--ADLSLLDRNGNSVLHLAAKE 621
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 344 REPKIIVSLITKARPADV-----TFQGRKAVQISKRLTKGGDYFGVTEGKPSPKDRLCI 399
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 622 GHDRII-SILLKSKAAPLDHPNGEGLNAHIA-----VMSNSLP-----CL 663
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 400 EIL-----EQARRDPOLGASVSLAMAGE--SLRGRLLYLENRVALARINFPMEARVMD 453
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 664 LLLVAAGAENVNAQEKSGRTPLHLAVEYDNISLAGCLL-----LEGDAHVD 709
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 454 IAQVDTGLENL-----GSGANPPPERQRTVDLINES 485
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 710 STTYDGTPLHIAAGRGSTRLLAALLKAAGADPLVENFEPLYDLDDSD 755
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
YGY4_HALSQ
ID YGY4_HALSQ STANDARD; PRT; 744 AA.
AC F21562;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL 80.2 KDA PROTEIN IN THE 5'REGION OF GYRA AND GYRB (ORF
DE 4).
OS Haloferax sp. (strain Aa 2.2).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Haloferax.
OX NCBI_TaxID=2254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91100352; PubMed=1846146;
RA Holmes M.L., Dylla-Smith M.L.;
RT "Mutations in DNA gyrase result in novobiocin resistance in
RT halophilic archaeobacteria.";
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RL J. Bacteriol. 173:642-648(1991).
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M38373; AAB09604.1; -
DR PIR; D39135; D39135.
KW Hypothetical protein.
SQ SEQUENCE 744 AA; 80236 MW; 2D466279A5A49DA3 CRC64;
```

```
Query Match 3.8%; Score 111; DB 1; Length 744;
Best Local Similarity 22.3%; Pred. No. 5.2;
Matches 115; Conservative 73; Mismatches 180; Indels 148; Gaps 24;

QY 31 VEALRRLSDNLAARFSPEDFAFLADARTAVPGGGGGGLRVHRCVLSARS-PFLRGVF 89
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 222 LEGONRELAVALALLGRPARGVALHDEQFGLRG-----VAALAVRELPRQGRF 270
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 90 ARRAAAA-----AGGGGDSERLELRLGGGEEVEGYEALRLVLDLYSGRV 140
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 271 ERGLAGELLGLRLGAGAGGLDG-----LR-----DGRRRRVLLERPELLV 315
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 141 GD-LPKAACLCVDEDAHVCHPAPVAFMAQVL-----FAASTFQVAELTNLFQ 187
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 316 GDALDDAADLGIPE-----LGLRLALELRVGVLDGDDGGESLANVLAEEVAVVQHVVA 371
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 RRLDVLVD-----KVEVDNLLILSVANLCKNCKMKLLERCLDMVVRN-----231
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 372 VRY--VYDDAGERLRLEPGQMRALAGVDVYVVEG-----VNRPLEVGLRHLGDFDLALRV 425
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 --LDMITLTKSLP-PDVIKIIDARLS-----LGLISPENKGFPPKHKVRIIRAL--DSD 281
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 426 VYDDVVVERLGLVEVDELDAALAEERARLVGLVGERNLDPGVEERELSQAVPERL 485
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 282 DVELVRLMT-----EGQTNLDDAFALHYAVEHCDSKITTELDLALADVNHRNPRGYT 335
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 486 EVELGRLEDTVVRPKADGRSGVFAGFEVAHAL-----ELLDLRLADLEAVCPHRAV 536
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 336 VLHI---AARRREPK-----IIVSL-----LTKGA-----RP 359
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 537 VFOLDPEFAKQVRVDDGDADAVEAAGDLVGLVPELPAGVEDGDDQLQRGSVVLFVRYRNP 596
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 360 ADVTFGGRKAVQISKRLTKGGDYFGVT---EEGKPSPKDRLCIETLELQAEARRDPOLGEAS 416
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 597 AAVVGDAADRAVLV-----EGDLDGVAVARERLVGDVDDFVDEVESARIGGPDVHRT 650
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 417 VS---LAMAGESLRLLYLENVALARINFPMEAR 449
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 651 LSNQGFPPEDNLSGPVLVILRLHNRPRIARPLKAR 686
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: July 12, 2001, 17:14:54  
Job time: 135 sec

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7

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2001, 17:12:38 ; Search time 19.52 seconds  
(without alignments)  
2271.188 Million cell updates/sec

Title: US-09-294-539-4

Perfect score: 2952

Sequence: 1 MEPPTHVNTAFSDSDASV.....RSLSSSSSTSGIAIRPR 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1276	43.2	593	F96666	hypothetical prote
2	1213.5	41.1	600	T04267	NPRI protein homol
3	985.5	33.4	601	T04747	hypothetical prote
4	441.5	15.0	467	T47773	hypothetical prote
5	421	14.3	491	H84840	hypothetical prote
6	132.5	4.5	4377	A55575	ankyrin 3, long sp
7	131.5	4.5	1016	T19006	ankyrin related pr
8	131	4.4	1856	B35049	ankyrin 1, erythro
9	131	4.4	1880	A35049	ankyrin 1, erythro
10	131	4.4	1881	1 SJHUK	ankyrin 1, erythro
11	128.5	4.4	1943	T42713	ankyrin 3, splice
12	128	4.3	1848	T37771	ankyrin, erythrocy
13	127	4.3	1765	T42714	ankyrin 3, splice
14	127	4.3	1940	T42715	ankyrin 3, splice
15	127	4.3	1961	T42716	ankyrin 3, splice
16	127	4.3	3924	T37431	ankyrin 2, neurona
17	126.5	4.3	543	C86212	hypothetical prote
18	125.5	4.3	532	G84427	hypothetical prote
19	123	4.2	1862	T49502	ankyrin - mouse
20	122.5	4.1	331	T01838	hypothetical prote
21	122	4.1	466	T33574	hypothetical prote
22	120.5	4.1	984	A41996	NF-kappa-B p50 sub
23	119.5	4.0	359	A55839	transcription fact
24	119	4.0	1963	1 MKW	myosin heavy chain
25	119	4.0	2352	T30201	Notch homolog prot
26	117.5	4.0	907	T15044	p50B/p97 (lyt-10)
27	117	4.0	211	T18174	ankyrin repeat pro
28	117	4.0	1188	T28396	chromosome segrega
29	116.5	3.9	323	B47169	ankyrin-like repea

#### ALIGNMENTS

RESULT 1

F96666

hypothetical protein F15H21.6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: F96666

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
Chin, C.W.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: F96666

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-593 <STO>

A:Cross-references: GB:AE005173; NID:g10645392; PIDN:AG21510.1; GSPDB:GN00141

C:Genetics:

A:Gene: F15H21.6

A:Map position: 1

Query Match

Best Local Similarity 43.2%; Score 1276; DB 2; Length 593;

Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSDASVEEGDADADVEALRLSDNLAAAFSPEDFAFLADARIAVPGG 64

Db 17 TSFVATDNTDSSIVLAEEQVLTGPDVSALQLLSNFESVFSDPD--FYSDAKLVL--- 71

QY 65 GGGGDLRVHRCVLSARSFELRCVFAARRAAAGGGEDGSERLLELLGGGEEVEVG 124

Db 72 -SDGREVSPHRCVLSARSFFFSALA--AAKKEKDSNNTAAVKLEKEI----AKDYEVG 124

QY 125 YBALRLVLDLYSGRVGDLPKAACLCVDECAHVGCHPAVAFMAQVLFDAASTFQVAELTN 184

Db 125 FDSVTVLAYVYSSRVPPKGVSECADENCCCHVACRPAYDFMFLVLYLAFIKFELIT 184

QY 185 LFORLLDLVKVEVDNLLLSVANLCKNCKMKLERCLDMVVRNLDMTITLESLLPPD 244

Db 185 LYQRHLLDVVDVWVIEDTLVILKLANICGACMKLLDRCKEIIIVKSNVDMVSLPEL 244

QY 245 VIKQIIDARLSLGLSPENKGFNKHVRHRAALSDSDVVELVRLMTEGTNLDLDAFALH 304

Db 245 LKKEIIDRRKELGLEVPKYK----KHVSNNVHKAALSDSDVVELVRLMTEGTNLDLDAFALH 300

QY 305 YAVEHCDSKITTELLDALADVNHNRNPRGTVTLHIAARRRREPKIIVSLTCKGARPADVTF 364

30 116.5 3.9 439 2 J01729 ankyrin-repeat pro  
31 116.5 3.9 781 2 S75367 zam protein - Syne  
32 114.5 3.9 1001 2 S30385 G9a protein - huma  
33 114 3.9 552 1 TWMT3 transforming prote  
34 113.5 3.8 854 2 S33558 unc-33 protein - C  
35 113.5 3.8 1283 2 T29109 histidine kinase F  
36 113 3.8 495 2 T27995 hypothetical prote  
37 112.5 3.8 1411 2 S30355 alpha-latroinsecto  
38 112.5 3.8 1786 2 A57282 ankyrin-related pr  
39 112.5 3.8 1815 2 T15346 elegans ankyrin-re  
40 112.5 3.8 1867 2 T15344 ankyrin-related un  
41 112.5 3.8 2039 2 T15347 ankyrin-related un  
42 112 3.8 397 2 T46445 hypothetical prote  
43 112 3.8 880 2 F75103 conserved hypothet  
44 112 3.8 1107 2 T21280 hypothetical prote  
45 112 3.8 1964 2 T09059 notch4 - mouse

Db 301 FAVAYCNKATATDLLKDLADVNHRNPRGYTVLHVAAKRPQILSLLEKGAASEATL 360  
QY 365 DGRKAVOISRLTKQGDYFGVTEGKPSKDRCLCIETLEQAERDQOLGASVSLAMAGE 424  
Db 361 EGRALMAIAKQATMAVCNNINPEQCKHSLKGLRCVETLEQEDREQIPRDVPPSFVAAD 420  
QY 425 SLGRLLYLENVALARIMFPMARVAMDIAQDGTGLEFNLSGANGPPPP---ORTTV 480  
Db 421 ELKMTLDLENVALAQRLEPTEAQAAMEAKMGCEFIIVTS---LEPRLTGTRKTS 477  
QY 481 DLNESPIMKEEHLARMTALSKTVELGKFRPPRCNSVLDKIMD-DETDPVSLGRDTS 539  
Db 478 GVKIAPPRILEEHQSLKALSKTVELGKFRPPRCNSVLDKIMD-DETDPVSLGRDTS 537  
QY 540 R----KRFHLDQVLQKAFHEDKEENDRSGLSSSSSTS 574  
Db 538 LKQKQRYMEIQETLKAFSEDNLELGNSSLTDTSTSTS 576

RESULT 2  
T04267  
NPRI protein homolog F20B18.230 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 30-Apr-1999  
C:Accession: T04267  
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, March 1999  
A:Reference number: Z15263  
A:Accession: T04267  
A:Molecule type: DNA  
A:Residues: 1-600 <BEV>  
A:Cross-references: EMBL:AL049483  
A:Experimental source: cultivar Columbia; BAC clone F20B18  
C:Genetics:  
A:Map position: 4  
A:Introns: 186/3; 433/1; 501/1  
A:Note: F20B18.230

Query Match 41.1%; Score 1213.5; DB 2; Length 600;  
Best Local Similarity 45.8%; Pred. No. 7e-76;  
Matches 277; Conservative 105; Mismatches 172; Indels 51; Gaps 17;

QY 1 MEPTTSHVTFNAPSASVEEG---ADADAD-----VEALRLSDNLAAAFR 46  
Db 1 MATTTTITARFSDSYEFNTSGNSFFAESLDYPTFEULTPPEVSALKLLNCSLESVF 60

QY 47 SPEDFAFLADARIAVPGGGGGDLRVHRCVLSARSFPLRGVFAARRAAAGGGEGDGE 106  
Db 61 SPE--TFYSDAKLVL---AGGREVSFHCILSARIP---VF--KSALATVKEQKSTTV 109

QY 107 RLRLRELLGGGGEVEGYEALRLVLDYLSGRVGDLPKAACLVDEDCAHVGCHPAVAF 166  
Db 110 KLQKUEI---ARDYEGVDFSVAVLAIVYSGRVSPKASACVDDCCCHVACRSKVD 165

QY 167 MAQVFAASTFQVAELTNLFQRLLDVLKVEVDNLLILSVANLCKSMKLLERCLDM 226  
Db 166 MVEVYLVSFVQIQELVTLVYERQFLEIVDKVWVEDILVFELDLTCGTYTKLLDRCEI 225

QY 227 VVRNLMITLESPLPDVTKIITDAKLSGLISPENKGFNKHVRIHRAALSDDDVELV 286  
Db 226 IVKSDIELVLSLEKSLPQHFQIIDIREALCLEPPKLE---RHVKNIYKALSDDDVELV 281

QY 287 RMLLTGOTNLDLAFALHYAVEHCDSKITTELDLADLVNHRNPRGYTVLHIAARREP 346  
Db 282 KMLLEGTNLDLAFALHYAVEHCDSKITTELDLADLVNHRNPRGYTVLHIAARREP 341

QY 347 KIIIVSLTKGARPADVTFDGRKAVQISKRLLTKQGDYFGVTEGKPSKDRCLCIETLEQA 406  
Db 342 KLIISLLMKGANILDTLTDGRALTALVIVKRLTKADDTSTEDGTPSLKGGCIEVLEH-E 400

QY 407 RRDQPLG--EASVSLAMAGESLRRLYLENVALARIMFPMARVAMDIAQDGTGLEFN 464

Db 401 QKLEYLSPEASLSLPTPEELRMRLLYENRVALARLLFPVETVQGIKLEETCEFT 460  
QY 465 LGSANGPPPE--RQRTVDLINESPFFIMKEEHLARMTALSKTVELGKFRPPRCNSVLDKIM 522  
Db 461 -ASSLEPDDHHIGKRTSLDINMAPFQIHEKHLRLKALCKTVELGKRYFKRCS--LDHEM 517  
QY 523 DDE--TDPVSLGRDT---SAEKKRPFHLDQVLQKAFHEDKEENDRSGLSSSSSTSIGA 577  
Db 518 DTEDLNLHASVEEDTPEKRLQKQRYMELQETLMKTFSEDKEE---CGKSSSTPKPTS--A 572

QY 578 IRPRR 582  
Db 573 VRSNR 577

RESULT 3  
T04747  
hypothetical protein T16H5.20 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-Jun-1999  
C:Accession: T04747  
R:Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Bancroft, I.; Mewes, H.W.; May  
submitted to the Protein Sequence Database, June 1998  
A:Reference number: Z15383  
A:Accession: T04747  
A:Molecule type: DNA  
A:Residues: 1-601 <BEV>  
A:Cross-references: EMBL:AL024486  
A:Experimental source: cultivar Columbia; BAC clone T16H5  
C:Genetics:  
A:Map position: 4  
A:Introns: 173/3; 420/1  
A:Note: T16H5.20

Query Match 33.4%; Score 985.5; DB 2; Length 601;  
Best Local Similarity 40.8%; Pred. No. 3.5e-60;  
Matches 242; Conservative 96; Mismatches 170; Indels 85; Gaps 18;

QY 34 LRLRLSDNLAAAFRSPEDFAFLADARIAVPGGGGGDLRVHRCVLSARSFPLRGVFAARR 92  
Db 35 LEELSSNLEQLLTNPDCDY---TDAELIIE---EENPVSVHRCVLAARSKFFLDLFFK- 87

QY 93 AAAAAAGGGEGDGE---RLRLRELLGGGGEVEGYEALRLVLDYLSGRVGDLPKAAACL 149  
Db 88 -----DKDSSEKKPKYQMKDLLPYG---NVGREAFHLFLSYITGRKPPPIEVST 135

QY 150 CVDEDCAHVGCHPAVAFMAQVLFPAASTFQVAELTNLFQRLLDVLKVEVDNLLILSVA 209  
Db 136 CVDSVCAHDSCKPAIDPAVELMYASFVQIPDLVSSFORKLRNVKESLVENLPIILVA 195

QY 210 NLCKSMKLLERCLDMVVRNLMITLESPLPDVTKIITDAKLSGLISPENKGFN 268  
Db 196 FHCULT---QLDQCIEVARSDDDRFCIEKLEPVELEKIKQLRVKSVNPIPEDEKSI-- 251

QY 269 KHVRIHRAALSDDDVELVRLMLLTGEGQTNLDFALHYAVEHCDSKITTELDLADLVN 328  
Db 252 ERTGKVLKALSDDDVELVRLMLLTGEGQTNLDFALHYAVEHCDSKITTELDLADLVN 311

QY 329 RNPFGYTVLHIAARREPPIIVSLLTGKARPADVTFDGRKAVQISKRLLTKQGDYFGVTEE 388  
Db 312 RNSRGYTVLHIAARREPPIIVSLLTGKARPADVTFDGRKAVQISKRLLTKQGDYFGVTEE 371

QY 389 GKSPKDRCLCIETLEQAERDQOLGASVSLAMAGESLRRLYLENVALARIMFPM 447  
Db 372 KEPS-KYRLCIDILEREIRNPLVSGDTPPCSHMPEDQLMRLYLEKRVGLAQLPFAE 430

QY 448 ARVAMDAQVDGTLLEFNLSGANGPPPPRQRT-----VDLNESEPFIMKEEHLARMTALSK 502  
Db 431 ANVAMDVANVESTSEC---TGLLTPPPSNDTLENLGVLDNETPYVQTKRMLTRKMLK 487

QY 503 T-----VELGKFRPPRCNSVLDKIMD---DETDPVSLG 532



Db 488 TCKSLRCKTFKFSYLTTRLTDSKPFNNVAVETGRRYFPSCYEVLDKYMDOYMEIP---- 543  
QY 533 RTSS-----AKKRRFHDLDVLOKAFHEKDEKNDKSLSSSSSTSI 575  
Db 544 -DMSYPEKGTVKRQKRMRYNELNDVKKAYSQDKVA--RSLSSSPASSL 593

## RESULT 4

T47773

hypothetical protein F2413.210 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C:Accession: T47773

R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;

submitted to the Protein Sequence Database, February 2000

A:Reference number: 224475

A:Accession: T47773

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-467 &lt;NYA&gt;

A:Cross-references: EMBL:AL138655

A:Experimental source: cultivar Columbia; BAC clone F2413

C:Genetics:

A:Map position: 3

A:Introns: 157/3

A:Note: F2413.210

Query Match 15.0%; Score 441.5; DB 2; Length 467;  
Best Local Similarity 30.8%; Pred. No. 7.2e-23;  
Matches 137; Conservative 72; Mismatches 169; Indels 67; Gaps 16;

QY 32 EALRRLS---DNLAAFRSPEDFAFLADARIAVPGGGGGDLRVHRCVLSARSFPLRGV 88  
Db 7 ELSKNSLDYLNLLINGQAFSDVTFSEVGR-----VHAHRCILAAARSLEFRKF 55  
QY 89 FARRAAAAAGG---GGDGERLELRLGGGEEV---EVGYEALRLVDLYSGRGVDLP- 144  
Db 56 FCESDSPQGAEPANGTGS---GARAAGVGVPVNSGYEVFELLQLLYSGQVSIVPH 112  
QY 145 --KAACLCVDECAHVCHPVAFAQVLFPAASTFOVAELTNLFORRLDLVDKVEVDNL 202  
Db 113 KHEPRNCGDRGCHWTHCTAAVDLSLDILAAARYFCVEQLALLTQKHLTSMVEKASIEDV 172  
QY 203 LLILSVANLCNCKMKLLERCCLDMVVRNLDMTLEKSLPPDVVKOIIDARLSGLISPE 262  
Db 173 MKVLIASR--KQDMHQLWTTCSTLYIAKSGLPQEIILAKHLPIELVAKIEELRKSSM--PL 228  
QY 263 NKGFPNKH-----VRRIRHALSDSDVELVRLMLTTEGQTNLDLDAFALHVAHEHC 310  
Db 229 RSLMPHHDLTSTLDLEDQKIRMRRLDSSDVELVRLMVGEGNLDLSALIYAVENC 288  
QY 311 DSKITTELLDLADLVNH--RNPRGYTVLHIAARRRPEKIIIVSLITKGARPADVTFDRKA 369  
Db 289 SREVKALLEGAADVNYVPAGPTGKTALHIAAEMVSPDMVAVLLDDHDPNVQTVGDIPT 348  
QY 370 VQISKRLTK-----QGYDFGVTEGKSPKDRICIEILEOA-----ERRD----- 409  
Db 349 LDILRLTSDFLFKGAIPGLTHI-EPN-KLRCLCLELVQSAALVISREEGNNNSNDNNTMI 406  
QY 410 -POLGEASVSLAMAGSLRLLYL 433  
Db 407 YPMKDEHTS-----GSSLDLSRLVYL 427

## RESULT 5

H84840

hypothetical protein At2g41370 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: H84840

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: H84840  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-491 <STO>  
A:Cross-references: GB:AE002093; NID:g3894187; PIDN:AACT8536.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g41370  
A:Map position: 2

Query Match 14.3%; Score 421; DB 2; Length 491;  
Best Local Similarity 29.2%; Pred. No. 2e-21;  
Matches 135; Conservative 72; Mismatches 170; Indels 86; Gaps 15;

QY 32 EALRRLS---DNLAAFRSPEDFAFLADARIAVPGGGGGDLRVHRCVLSARSFPLRGV 88  
Db 6 ELSRLSLDLFNLINGQAFSDVTFSEVGR-----VHAHRCILAAARSLEFRKF 54  
QY 89 FARRAAAAAGGCGDGERLELRLGGGEEV-----EVGYEALRLVL 132  
Db 55 FC-----GTDSPQPVGTGIDPTQHGSPASPTRGSTAPAGIIPVNSGVYEVFLLLL 104  
QY 133 DYLSGRVGDLP---KAACLCVDECAHVCHPVAFAQVLFPAASTFOVAELTNLFQRR 189  
Db 105 QFLYSGQVSIVPQKHEPRNCGERGCHWTHCTAAVDLSDILAAARYFCVEQLALLTQK 164  
QY 190 LLDVLDKVEVDNLTLTSLVANLCNCKMKLLERCCLDMVVRNLDMTLEKSLPPDVVKOI 249  
Db 165 LASWEEKASIEDVMKVLIASR--KQDMHQLWTTCSTLYIAKSGLPQEIILAKHLPIDVVTKI 222  
QY 250 IDARLSGL-----KGFNKHVRRIRHALSDSDVELVRLMLTTEGQTNL 297  
Db 223 EELRLKSSITARRSLMPHHHDLSDVAQDLEDQKIRMRRLDSSDVELVRLMVGEGNLL 282  
QY 298 DDAFALHYAVECHDCKITTELLDLADLVNH--RNPRGYTVLHIAARRRPEKIIIVSLITKG 356  
Db 283 DESLALHYAVESCSEVVKALLEGAADVNYVPAGPTGKTALHIAAEMVSPDMVAVLLDDH 342  
QY 357 ARPADVTFGKRAVQISKRLTK---QGYDFGVTEGKSPKDRICIEILEOA----- 405  
Db 343 ADPNVTGCGIPLDLRLTSDFLFKGAVPGLTHI-EPN-KLRCLCLELVQSAAMVISRE 400  
QY 406 -----ERRD-----POLGEASVSLAMAG--ESLRGLLYL 433  
Db 401 EGNNSNNQNDNNTGIYPHMNEHNSGSGSNNNLDLSRLVYL 443

## RESULT 6

A55575

ankyrin 3, long splice form - human

N:Alternate names: ankyrin G

C:Species: Homo sapiens (man)

C&gt;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 20-Sep-1999

C:Accession: A55575

R:Kordeli, E.; Lambert, S.; Bennett, V.

J. Biol. Chem. 270, 2352-2359, 1995

A:Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the

A:Reference number: A55575; MUID:95138209

A:Accession: A55575

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-4377 &lt;KOR&gt;

A:Cross-references: GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025

C:Genetics:

A:Gene: GDB:ANK3

A:Cross-references: GDB:424503; OMIM:600465

A:Map position: 10q21-10q21

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol



C: Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 10-Jul-1998  
 R: Accession: B35049  
 R: Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;  
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
 A: Title: cDNA sequence for human erythrocyte ankyrin.  
 A: Reference number: A35049; MUID: 90175370

A: Accession: B35049  
 A: Status: preliminary  
 A: Molecule type: mRNA  
 A: Residues: 1-1856 <LAM>  
 C: Genetics:  
 A: Gene: GDB: ANK1; ANK  
 A: Cross-references: GDB: 118737; OMIM: 182900  
 A: Map position: 8p11.2-8p11.2  
 C: Superfamily: ankyrin; ankyrin repeat homology  
 C: Keywords: alternative splicing  
 F: 2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>  
 F: 2-1513/1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
 F: 44-76/Domain: ankyrin repeat homology <AN01>  
 F: 77-109/Domain: ankyrin repeat homology <AN02>  
 F: 110-142/Domain: ankyrin repeat homology <AN03>  
 F: 143-171/Domain: ankyrin repeat homology <AN04>  
 F: 172-204/Domain: ankyrin repeat homology <AN05>  
 F: 205-237/Domain: ankyrin repeat homology <AN06>  
 F: 238-270/Domain: ankyrin repeat homology <AN07>  
 F: 271-303/Domain: ankyrin repeat homology <AN08>  
 F: 304-336/Domain: ankyrin repeat homology <AN09>  
 F: 337-369/Domain: ankyrin repeat homology <AN10>  
 F: 370-402/Domain: ankyrin repeat homology <AN11>  
 F: 403-435/Domain: ankyrin repeat homology <AN12>  
 F: 436-468/Domain: ankyrin repeat homology <AN13>  
 F: 469-501/Domain: ankyrin repeat homology <AN14>  
 F: 502-534/Domain: ankyrin repeat homology <AN15>  
 F: 535-567/Domain: ankyrin repeat homology <AN16>  
 F: 568-600/Domain: ankyrin repeat homology <AN17>  
 F: 601-633/Domain: ankyrin repeat homology <AN18>  
 F: 634-666/Domain: ankyrin repeat homology <AN19>  
 F: 667-699/Domain: ankyrin repeat homology <AN20>  
 F: 700-732/Domain: ankyrin repeat homology <AN21>  
 F: 733-765/Domain: ankyrin repeat homology <AN22>  
 F: 766-798/Domain: ankyrin repeat homology <AN23>

Query Match 4.4%; Score 131; DB 2; Length 1856;  
 Best Local Similarity 23.6%; Pred. No. 1-2;  
 Matches 75; Conservative 34; Mismatches 103; Indels 106; Gaps 12;

QY 271 VRRHRLDSDDDVELVRLMLT-----EGQTNLDDAF----- 301  
 DB 636 VTPHLAAQGEAHEMVALLSKQANGNLGNKSGLTPLHLVAQGHVPADVLIKHGVMVD 695  
 QY 302 -----ALHYAVEHCDSKITTELLDALADYNHNRPRGYTVLHIAARREPKIIVSLL 353  
 DB 696 ATTRMGVTPPLHVAHYGNIKLVKFLQ-HQADYNNAKTGLGYSPLHQAQOQGHDTIVTLL 754  
 QY 354 TKGARPADVTFDGRKAVQISKRLTKQGDYFGVTEEG-----PSPKDRLCI----- 399  
 DB 755 KNGASPNVSSDGTTPPLAIKRL-----GYISVTDVLKVVTDTSFVLVSKHRMSPETV 810  
 QY 400 -EILEQARERDPOLGEASVSLAMAGESLRGLLYLENVALARIMPFMEARVAMDIQVD 458  
 DB 811 DEILDVSEDE-----GEEL-----ISFKAERDRSDVDEEK 841  
 QY 459 GTLEFNLGSGANPPPERQRTTVDNLNESPFTMKBEHLARMTALSKTVELGKRFPPRCNVL 518  
 DB 842 ELLDF-----VPKLDQVV-----ESPAIPRI-----CAMPETVVIRSEEQASKEY 884  
 QY 519 DKTMDDTDPVSLGRDTS 536  
 DB 885 D-----EDSLIPSPATETS 899

RESULT 9

A35049  
 ankyrin 1, erythrocyte splice form 2 - human  
 N: Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
 N: Contains: ankyrin 2.2, erythrocyte  
 C: Species: Homo sapiens (man)  
 C: Date: 27-Jul-1990 #sequence\_revision 01-Oct-1992 #text\_change 04-Sep-1998  
 R: Accession: A35049  
 R: Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;  
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
 A: Title: cDNA sequence for human erythrocyte ankyrin.  
 A: Reference number: A35049; MUID: 90175370

A: Accession: A35049  
 A: Status: preliminary  
 A: Molecule type: mRNA  
 A: Residues: 1-1880 <LAM>  
 A: Cross-references: GB: M28880  
 C: Genetics:  
 A: Gene: GDB: ANK1; ANK  
 A: Cross-references: GDB: 118737; OMIM: 182900  
 A: Map position: 8p11.2-8p11.2  
 C: Superfamily: ankyrin; ankyrin repeat homology  
 C: Keywords: alternative splicing; cytoskeleton  
 F: 2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>  
 F: 2-1513/1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
 F: 44-76/Domain: ankyrin repeat homology <AN01>  
 F: 77-109/Domain: ankyrin repeat homology <AN02>  
 F: 110-142/Domain: ankyrin repeat homology <AN03>  
 F: 143-171/Domain: ankyrin repeat homology <AN04>  
 F: 172-204/Domain: ankyrin repeat homology <AN05>  
 F: 205-237/Domain: ankyrin repeat homology <AN06>  
 F: 238-270/Domain: ankyrin repeat homology <AN07>  
 F: 271-303/Domain: ankyrin repeat homology <AN08>  
 F: 304-336/Domain: ankyrin repeat homology <AN09>  
 F: 337-369/Domain: ankyrin repeat homology <AN10>  
 F: 370-402/Domain: ankyrin repeat homology <AN11>  
 F: 403-435/Domain: ankyrin repeat homology <AN12>  
 F: 436-468/Domain: ankyrin repeat homology <AN13>  
 F: 469-501/Domain: ankyrin repeat homology <AN14>  
 F: 502-534/Domain: ankyrin repeat homology <AN15>  
 F: 535-567/Domain: ankyrin repeat homology <AN16>  
 F: 568-600/Domain: ankyrin repeat homology <AN17>  
 F: 601-633/Domain: ankyrin repeat homology <AN18>  
 F: 634-666/Domain: ankyrin repeat homology <AN19>  
 F: 667-699/Domain: ankyrin repeat homology <AN20>  
 F: 700-732/Domain: ankyrin repeat homology <AN21>  
 F: 733-765/Domain: ankyrin repeat homology <AN22>  
 F: 766-798/Domain: ankyrin repeat homology <AN23>

Query Match 4.4%; Score 131; DB 2; Length 1880;  
 Best Local Similarity 23.6%; Pred. No. 1-2;  
 Matches 75; Conservative 34; Mismatches 103; Indels 106; Gaps 12;

QY 271 VRRHRLDSDDDVELVRLMLT-----EGQTNLDDAF----- 301  
 DB 636 VTPHLAAQGEAHEMVALLSKQANGNLGNKSGLTPLHLVAQGHVPADVLIKHGVMVD 695  
 QY 302 -----ALHYAVEHCDSKITTELLDALADYNHNRPRGYTVLHIAARREPKIIVSLL 353  
 DB 696 ATTRMGVTPPLHVAHYGNIKLVKFLQ-HQADYNNAKTGLGYSPLHQAQOQGHDTIVTLL 754  
 QY 354 TKGARPADVTFDGRKAVQISKRLTKQGDYFGVTEEG-----PSPKDRLCI----- 399  
 DB 755 KNGASPNVSSDGTTPPLAIKRL-----GYISVTDVLKVVTDTSFVLVSKHRMSPETV 810  
 QY 400 -EILEQARERDPOLGEASVSLAMAGESLRGLLYLENVALARIMPFMEARVAMDIQVD 458  
 DB 811 DEILDVSEDE-----GEEL-----ISFKAERDRSDVDEEK 841  
 QY 459 GTLEFNLGSGANPPPERQRTTVDNLNESPFTMKBEHLARMTALSKTVELGKRFPPRCNVL 518  
 DB 842 ELLDF-----VPKLDQVV-----ESPAIPRI-----CAMPETVVIRSEEQASKEY 884

Qy 519 DKIMDDETPVSLGRDTS 536  
| : | | : ||  
Db 885 D---EDSLIPSSPATETS 899

## RESULT

STHUK

ankyrin 1, erythrocyte splice form 1 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: ankyrin 2.2  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 22-Jun-1999  
C:Accession: S08275; A33219; PC2220; A35443  
R:Lux, S.E.; John, K.M.; Bennett, V.  
Nature 344, 36-42, 1990  
A:Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure w  
A:Reference number: S08275; MUID:90158830  
A:Accession: S08275  
A:Molecule type: mRNA  
A:Residues: 1-1881 <LU1>  
A:Cross-references: EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702  
A:Accession: A33219  
A:Molecule type: protein  
A:Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30:733-749, 'A', 751-753:828-833, 'X', 835-855, 'X',  
X', 1367:1383-1427:1601-1630:1686-1698, 'D', 1700:1763-1772 <LUX>  
A:Note: 845-Arg and 1392-Thr were also found  
R:Hermann, J.; Barel, M.; Frade, R.  
Biochem. Biophys. Res. Commun. 204, 453-460, 1994  
A:Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane  
A:Reference number: PC2220; MUID:95071348  
A:Accession: PC2220  
A:Molecule type: protein  
A:Residues: 910-929 <HER>  
R:Davis, L.H.; Bennett, V.  
J. Biol. Chem. 265, 10589-10596, 1990  
A:Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger  
A:Reference number: A35443; MUID:90285190  
A:Accession: A35443  
A:Molecule type: protein  
A:Residues: 'X', 5, 'X', 7-12:403-417, 'X', 419-422, 'H', 424, 'LQ', 797-800, 'L', 802-814:862-863,  
C:Genetics:  
A:Gene: GDB:ANK1; ANK  
A:Cross-references: GDB:118737; OMIM:182900  
A:Map position: 9p11.2-9p11.2  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing; phosphoprotein  
F:2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>  
F:2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>  
F:2-827/Domain: 89K #status predicted <DOM1>  
F:2-827/Region: anion exchange protein binding  
F:44-76/Domain: ankyrin repeat homology <AN01>  
F:77-109/Domain: ankyrin repeat homology <AN02>  
F:110-142/Domain: ankyrin repeat homology <AN03>  
F:143-171/Domain: ankyrin repeat homology <AN04>  
F:172-204/Domain: ankyrin repeat homology <AN05>  
F:205-237/Domain: ankyrin repeat homology <AN06>  
F:238-270/Domain: ankyrin repeat homology <AN07>  
F:271-303/Domain: ankyrin repeat homology <AN08>  
F:304-336/Domain: ankyrin repeat homology <AN09>  
F:337-369/Domain: ankyrin repeat homology <AN10>  
F:370-402/Domain: ankyrin repeat homology <AN11>  
F:403-435/Domain: ankyrin repeat homology <AN12>  
F:436-468/Domain: ankyrin repeat homology <AN13>  
F:469-501/Domain: ankyrin repeat homology <AN14>  
F:502-534/Domain: ankyrin repeat homology <AN15>  
F:535-567/Domain: ankyrin repeat homology <AN16>  
F:568-600/Domain: ankyrin repeat homology <AN17>  
F:601-633/Domain: ankyrin repeat homology <AN18>  
F:634-666/Domain: ankyrin repeat homology <AN19>  
F:667-699/Domain: ankyrin repeat homology <AN20>  
F:700-732/Domain: ankyrin repeat homology <AN21>  
F:733-765/Domain: ankyrin repeat homology <AN22>  
F:766-798/Domain: ankyrin repeat homology <AN23>

```
F:828-1382/Domain: 62K #status predicted <DOM2>
F:828-1382/Region: spectrin binding
F:1383-1881/Domain: 55K #status predicted <DOM3>
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Query Match 4.4%; Score 131; DB 1; Length 1881;  
Best Local Similarity 23.6%; Pred. No. 1.2;

Qy	271	VRRIHALDSDSDVELYRMLLT-----EGQTNLDADF-----	301
Db	636	VTPLHLAAQEGHAEWVALLSSKOANGNLGNKSGLTPLHLVAQGVHPVADVLIKHWGMYD	695
Qy	302	-----ALHYAVECHDSKITTELLDLALADYNHRNPRGYTVLHIAARRRREPKIIVSLL	353
Db	696	ATTBGMGYTPLHVASHYGNIKLVKFLQ-QHADVNAKTKLGYSPLHQAAQOGHTDIVTLLL	754
Qy	354	TKGARPADVTFDEGKAVOISKRLTKOGDYFGVTEEGK-----PSPKRLCI-----	399
Db	755	KNGASPNESVSDGTTPLUAIKRL-----GYLSVDVLKVVTDFTSVLVSOKHRRMSPETV	810
Qy	400	-EILEQEARDPQLGEASVSLAMAGESLRGLLLYLENRVALRIMPFEARVAMDIAQVD	458
Db	811	DEILDVSEDE-----GEEL-----ISFKAERDRSRDVDEEK	841
Qy	459	GTLEFNLGSGANPPPRQRTTVDLNESPFTMKEEHLARMTALSKTVGLGRFFPRCSNVL	518
Db	842	ELLDF-----VPKLDQVV-----ESPATPRIP-----CAMPETVVVIRSEEGEQASKEY	894
Qy	519	DKIMDDETDPVSLGROTS	536
Db	885	D---EDSLIPSSPATETS	899

## RESULT

T42713  
ankyrin 3, splice form 1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000  
C:Accession: T42713  
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo  
J. Cell Biol. 130, 313-330, 1995  
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin ge  
the repeat domain.  
A:Reference number: Z22237; MUID:95340633  
A:Accession: T42713  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1943 <PET>  
A:Cross-references: EMBL:L40632; NID:g710548; PID:g710550; PIDN:AAB01606.1  
A:Experimental source: strain C57BL/6J; kidney  
C:Genetics:  
A:Gene: Ank3  
A:Map position: 10  
A:Introns: 855/1  
C:Function:  
A:Description: supposed to play an important role in the polarized distribution of ma  
A:Note: major kidney ankyrin  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing

Query Match 4.4%; Score 128.5; DB 2; Length 1943;  
Best Local Similarity 23.8%; Pred. No. 1.8;

254 LSLGLISPENKGFNFKH-VRRIRHALSDDDVELVRMLLTGEG-----QTNLDDFAALHYAV 3070  
663 VSLLSRNANYNLNKSGLTFLHAAQEDRVNVAEVLVINGQAHVDAQTKMGYT-PLHVGCG 7210  
308 EHCDSKIITTELLDALADVNHRNPRGVTVLHIAARRREPKEIIIVSLLTGKARPADVTFDGR 3670  
722 HYGNIKIVNFLQHS-AKVNAKTNGYTTALHQAAGOGTHIIVLLONNNAAPNELTVNGN 7800

```
QY 368 KAVQISKRL----- 376
|:|:|
Db 781 TALAIARLGYISVDTLKVVTETMTTITTEKHKMNPETMNEVLNDSDDSEVRKASAP 840
QY 377 --TKQDGYFGVTEGKPS-----PKDRLCIEILEQAERRDPOLGEASVSLAMAGE 424
|:|:|
Db 841 EKLSDGEYISDGEEDAIITGDTKVLGPQD-----LKELGDDSLPAEGYVGFSLGARS 895
QY 425 SLR---GRLLYLENVALAR 441
|:|:|
Db 896 SLRSFSDRSYTLNRSSYAR 915

RESULT 12
S37771
Ankyrin, erythrocyte - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
C:Accession: S37771
R:Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J. Biol. Chem. 268, 9533-9540, 1993
A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found am
A:Reference number: S37771; MUID:93252825
A:Accession: S37771
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-184 <BIR>
A:Cross-references: EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:81-113/Domain: ankyrin repeat homology <AN01>
F:114-175/Domain: ankyrin repeat homology <AN02>
F:147-175/Domain: ankyrin repeat homology <AN03>
F:176-208/Domain: ankyrin repeat homology <AN04>
F:209-241/Domain: ankyrin repeat homology <AN05>
F:242-274/Domain: ankyrin repeat homology <AN06>
F:275-307/Domain: ankyrin repeat homology <AN07>
F:308-340/Domain: ankyrin repeat homology <AN08>
F:341-373/Domain: ankyrin repeat homology <AN09>
F:374-406/Domain: ankyrin repeat homology <AN10>
F:407-439/Domain: ankyrin repeat homology <AN11>
F:440-472/Domain: ankyrin repeat homology <AN12>
F:473-505/Domain: ankyrin repeat homology <AN13>
F:506-538/Domain: ankyrin repeat homology <AN14>
F:539-571/Domain: ankyrin repeat homology <AN15>
F:572-604/Domain: ankyrin repeat homology <AN16>
F:605-637/Domain: ankyrin repeat homology <AN17>
F:638-670/Domain: ankyrin repeat homology <AN18>
F:671-703/Domain: ankyrin repeat homology <AN19>
F:704-736/Domain: ankyrin repeat homology <AN20>
F:737-769/Domain: ankyrin repeat homology <AN21>
F:770-802/Domain: ankyrin repeat homology <AN22>

Query Match 4.3%; Score 128; DB 2; Length 1848;
Best Local Similarity 23.7%; Pred. No. 1.9;
Matches 58; Conservative 31; Mismatches 78; Indels 78; Gaps 8;

QY 271 VRRTHRALSDDDVLRMLLT-----EGQTNLDDAF----- 301
|:|:|
Db 540 VTPLHLAAQEGHTEWALLSLKQANGNLGNKSLGTLPLHLVYSEGHVPVADVILKHGVTVD 699
QY 302 -----ALHYAVEHCDSKITTELLDALADVNRHNRPRGYTVLHIAARREPKIIVSL 353
|:|:|
Db 700 ATTRMGVTPPLHVASHYGNIKLVKFLQ--HQADVNAKTKLGYSPHLQAQOQGHDTIVTLL 758
QY 354 TKGARPADVTDFGRKAVQISKRLTKQDGYFGVTEGK-----PSPKDLICI----- 399
|:|:|
Db 759 KNGASPNVSSNGTPTPLAIARL-----GYISVTDVLKVVTDTSVVLVSKHRMSYPET 814
QY 400 -EILEQAERRDPOLGEASVSLAMAGESLGRLLYLENVALARIMFPWEARVAMDIQVD 458
```

```
Db 815 DEILDYSE-----DEGTAHISIMGDELVS-----KAERRSDRDYGEK 853
QY 459 GTLEF 463
|:|
Db 854 ELLDF 858

RESULT 13
T42714
Ankyrin 3, splice form 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T42714
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin ge
the repeat domain.
A:Reference number: Z22237; MUID:95340633
A:Accession: T42714
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1765 <PET>
A:Cross-references: EMBL:L40632; NID:g710548; PID:g710551; PIDN:AAB01605.1
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 1587/1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 4.3%; Score 127; DB 2; Length 1765;
Best Local Similarity 32.6%; Pred. No. 2;
Matches 42; Conservative 20; Mismatches 59; Indels 8; Gaps 4;

QY 254 LSLGLISPENKGFNKH-VRRHRLSDSDVLRMLLTG-----QTNLDDAFALHYAV 307
|:|:|
Db 663 VSLLSRNANVNLNKSGLTPLHLAQEDRVNVAEVLVNOGAHVDAQTKMGYT-PLHVG 721
QY 308 EHCDSKITTELLDALADVNRHNRPRGYTVLHIAARREPKIIVSLLPKGARPADVTDFGR 367
|:|:|
Db 722 HYGNIKIVNELLQHS-AKVNAKTKNGYATLHQAQOQGHITINVLQNNASPNELTVNGN 780
QY 368 KAVQISKRL 376
|:|:|
Db 781 TALAIARRL 789

RESULT 14
T42715
Ankyrin 3, splice form 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T42715
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin ge
the repeat domain.
A:Reference number: Z22237; MUID:95340633
A:Accession: T42715
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1940 <PET>
A:Cross-references: EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604.1
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 834/1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
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Search completed: July 12, 2001, 17:14:01  
Job time: 83 sec



Qy 61 VPGGGGGGLRVHRCVLSARSPLRGVFAARRAAAAAGGGGGEDSERLELRELLGGGEE 120  
 Db 61 VPGGGGGGLRVHRCVLSARSPLRGVFAARRAAAAAGGGGGEDSERLELRELLGGGEE 120  
 Qy 121 VEVGYEARLRLVDLYSGRVGDLPKAACLCVDECAHVGCHPAVAFMAQVLFPAASTFQVA 180  
 Db 121 VEVGYEARLRLVDLYSGRVGDLPKAACLCVDECAHVGCHPAVAFMAQVLFPAASTFQVA 180  
 Qy 181 ELTNLFQRRLLDVLKVEVDNLLILSVANLCNCKMCKLLERCLDMVVRNLMITLEKS 240  
 Db 181 ELTNLFQRRLLDVLKVEVDNLLILSVANLCNCKMCKLLERCLDMVVRNLMITLEKS 240  
 Qy 241 LPPDVIKOIIDARLSGLISPENKGFNPKHVRRIHRAALSDVVELVRLMLTTEGOTNLDDA 300  
 Db 241 LPPDVIKOIIDARLSGLISPENKGFNPKHVRRIHRAALSDVVELVRLMLTTEGOTNLDDA 300  
 Qy 301 FALHYAVEHCDKSKITTELLDALADVNHRNPRGYTVLHIAARRREPKIIVSLLTKGARPA 360  
 Db 301 FALHYAVEHCDKSKITTELLDALADVNHRNPRGYTVLHIAARRREPKIIVSLLTKGARPA 360  
 Qy 361 DVTEDGRKAVOISKRLTKQGDYFGVTEEGKSPKDRLCIEILEQAERDPOLGEASVSLA 420  
 Db 361 DVTEDGRKAVOISKRLTKQGDYFGVTEEGKSPKDRLCIEILEQAERDPOLGEASVSLA 420  
 Qy 421 MAGESLRGLLYLENRVALARIMFPMPEARVAMIAQVDTGLEFNLGSGANPPPQRQRTTV 480  
 Db 421 MAGESLRGLLYLENRVALARIMFPMPEARVAMIAQVDTGLEFNLGSGANPPPQRQRTTV 480  
 Qy 481 DLNESPFTMKEEHLARMTALSKTVELGKRFPFRCNSVLDKIMDDTDPVSLGRDTSAEK 540  
 Db 481 DLNESPFTMKEEHLARMTALSKTVELGKRFPFRCNSVLDKIMDDTDPVSLGRDTSAEK 540  
 Qy 541 KRFHDLQVLOKAFHEDKEENDRSLGSSSSSTSGTGAIRPRR 582  
 Db 541 KRFHDLQVLOKAFHEDKEENDRSLGSSSSSTSGTGAIRPRR 582

RESULT 2  
 ID P93002 PRELIMINARY; PRT; 593 AA.  
 AC P93002; 004742;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE REGULATORY PROTEIN NPRI.  
 GN NPRI OR NTM1.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ECOTYPE COLUMBIA;  
 RX MEDLINE=97148688; PubMed=9019406;  
 RA Cao H., Glazebrook J., Clarke J.D., Volko S., Dong X.;  
 RA "The Arabidopsis NPRI gene that controls systemic acquired resistance  
 RT encodes a novel protein containing ankyrin repeats.";  
 RL Cell 88:57-63(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;  
 RA Ryals J., Weymann K., Lawton K., Friedrich L., Ellis D., Steiner H.Y.,  
 RA Johnson J., Delaney T.P., Jesse T., Vos P., Uknes S.;  
 RL Plant Cell 9:0-0(0).  
 DR EMBL; U76707; AAC49611.1;  
 DR EMBL; U87794; AAB58262.1;  
 DR Mende; 12931; Arath;2131;12931.  
 DR InterPro; IPR002110;  
 DR Pfam; PF00023; ank; 2.  
 DR Pfam; PF00651; BTB; 1.  
 DR PROSITE; PS50086; ANK\_REPEAT; 1.

DR PROSITE; PS50297; ANK\_REPEAT; 1.  
 DR PROSITE; PS50097; BTB; 1.  
 SQ SEQUENCE 593 AA; 66031 MW; DDD618146254CD68 CRC64;  
 Query Match 43.2%; Score 1276; DB 10; Length 593;  
 Best Local Similarity 47.2%; Pred. No. 3.2e-80;  
 Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;  
 Qy 5 TSHVTNFAFSDSDSASVEGDADADADVEALRRLSDNLAAAFSPEDFAFLADARIAPGG 64  
 Db 17 TSFVATDNTDSSIVYLAEEQVLTGPDYSALQLLSNFSFVDSPPD--FYSDAKLVL--- 71  
 Qy 65 GGGGGLRVHRCVLSARSPLRGVFAARRAAAAAGGGGGEDSERLELRELLGGGEEVEVG 124  
 Db 72 -SDGREVSFRCVLSARSSFFKSALA--AAKEDSNNTAAVKLEKEI-----AKDEVG 124  
 Qy 125 YEALRLVDLYSGRVGDLPKAACLCVDECAHVGCHPAVAFMAQVLFPAASTFQVAELTN 184  
 Db 125 FDSVTVTLAYVYSSKVRPPPKGVSECAENCHVACPAVDFMLEVLYLAFIKIPELIT 184  
 Qy 185 LFQRLDVLKVEVDNLLILSVANLCNCKMCKLLERCLDMVVRNLMITLEKSLLPPD 244  
 Db 185 LYQRLDVLKVEVDNLLILSVANLCNCKMCKLLERCLDMVVRNLMITLEKSLLPPD 244  
 Qy 245 VIKOIIDARLSGLISPENKGFNPKHVRRIHRAALSDVVELVRLMLTTEGOTNLDDAFALH 304  
 Db 245 LVKEIIDRRKGLLEVPEVK---KHVSNVHKAALSDSDIELVRLMLTTEGOTNLDDACALH 300  
 Qy 305 YAVEHCDKSKITTELLDALADVNHRNPRGYTVLHIAARRREPKIIVSLLTKGARPAVDTF 364  
 Db 301 FAVAVCNKVTATDLKLDLADVNHRNPRGYTVLHIAARRREPKIIVSLLTKGARPAVDTF 360  
 Qy 365 DGRKAVOISKRLTKQGDYFGVTEEGKSPKDRLCIEILEQAERDPOLGEASVSLAMAGE 424  
 Db 361 EGRALMIKATQAVTAVECNNIPEQCKHSLKGLRCLVEILEQEDKREQIPROVPPSFAVAAD 420  
 Qy 425 SLRGLLYLENRVALARIMFPMPEARVAMIAQVDTGLEFNLGSGANPPP---ORRTV 480  
 Db 421 ELKMTLLDLENRVALARIMFPMPEARVAMIAQVDTGLEFNLGSGANPPP---LEPDLRTGTKRTSP 477  
 Qy 481 DLNESPFTMKEEHLARMTALSKTVELGKRFPFRCNSVLDKIMDDTDPVSLGRDTSAEK 539  
 Db 478 GVKIAPFRILEHOSRLKALSKTVELGKRFPFRCNSVLDKIMDDTDPVSLGRDTSAEK 537  
 Qy 540 R---KRFHDLQVLOKAFHEDKEENDRSLGSSSSSTSGTGAIRPRR 574  
 Db 538 RLQKQRYMEIQETLTKAFSEDNLELGNSSLTDSSTSS 576

RESULT 3  
 ID Q9SZ13 PRELIMINARY; PRT; 600 AA.  
 AC Q9SZ13;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE NPRI LIKE PROTEIN.  
 GN F20B18.230 OR AT4G26120.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Rose M., Hempel S., Entian K.-D., Hoheisel J., Mewes H.W.,  
 RA Mayer K.F.X., Schueller C.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RA Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.



[3]  
 AC SEQUENCE FROM N.A.  
 RA Rose M., Hempel S., Entian K.-D., Meves H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RN SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL049483; CAB39677.1; -;  
 DR EMBL; AL161564; CAB79467.1; -;  
 DR InterPro; IPR000210; -;  
 DR InterPro; IPR002110; -;  
 DR Pfam; PF00651; BTB; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 DR PROSITE; PS50097; BTB; 1.  
 DR SMART; SM00248; ANK; 1.  
 SQ SEQUENCE 600 AA; 68006 MW; E32D3A1ED62ACB74 CRC64;  
  
 Query Match 41.1%; Score 1213.5; DB 10; Length 600;  
 Best Local Similarity 45.8%; Pred. No. 6.9e-76;  
 Matches 277; Conservative 105; Mismatches 172; Indels 51; Gaps 17;  
  
 QY 1 MEPPYSHVNTAFSDSDSASVEEGD-----ADADAD-----VEALRRRLSDNLAFAFR 46  
 DB 1 MATTTTITTTARSDSEFNTSGNFFAESSLDYPTFTPEVSALKLLSNCLESVFD 60  
  
 QY 47 SPEDFAFLADARAVPGGGGGDLVHRCVLSARSFPLRGVFAARRAAAGGGGGEDGSE 106  
 DB 61 SPE--TFYSDAKLVL-----AGGREVSFHRCLISARIP-----VF-KSALATVREKQSSTTV 109  
  
 QY 107 RLRLRELLGGGEEVGVYEAALRLDLXLSGRVGDLPKAAACLCYDVEDCAHVCHCPAVAF 166  
 DB 110 KLQKKEI-----ARDYEVGFDVVAVLAVYSGRVSPKPGSACVDVDDCHVACKSKVDF 165  
  
 QY 167 MAQVFAAFTFQVAELTNLFRRLDLVDKVEVDNLLILSVANLCNCKMCLLERCLDM 226  
 DB 166 MVEVLVLSFVQIQELVLYERQFLVDKVVVEDILVIFKLDTLGGTYKKLLDRCEII 225  
  
 QY 227 VVRSNDMTLEKSLPPDVIKQIIDARLGLTSPENKGFPPKHKVRRIRHALDSDVVELV 286  
 DB 226 IVKSDIELVLSLEKSLPQHIFKQIIDIREALCLEPPKLE-----RHVKNIYKALDSDVVELV 281  
  
 QY 287 RMLLTGQNLDDAFALHYAVEHCDCKYITTELLDLADLVNHNPRGYTVLHIAARRREP 346  
 DB 282 KMLLEGHNTLDEAYALHFAIACAVKATYDLELELADLVNLRNPRGYTVLHVAAMRKEP 341  
  
 QY 347 KIIVSLLTKGARPADVTDFGRKAVQISKRLTKOGDYFGVTEEGKPSPKDRLCIEILEQAE 406  
 DB 342 KLIISLUMKGANLDTLDRGTALVIVKRLTKADDTYKTDGTGTSKGLGCLIEVLEH-E 400  
  
 QY 407 RRDPPQLG--EASVSLAMAGESLRGLLYLENVALARIMFPMEARVAMDAVQDGTLEFN 464  
 DB 401 QKLEYLSPIEASLSLPTVPEELRMRLYYENVALARLLFPVETETVQGIKLEETCEFT 460  
  
 QY 465 LGSGANPPPE--RQRTVDLINESPFIKKEEHLARMTALSKTVELGKFRFPNCSNVLDKTM 522  
 DB 461 -ASSLEPDHIGKEKRTSLDNLNAPQIHEKHLISRLALCKTVELGKRYKRCGS--LDHPM 517  
  
 QY 523 DDE--TDPVSLGRDT--SAEKKRPHDLQDVLQKAFHEDKENDRSGLSSSSSTISICA 577  
 DB 518 DTEDLNHLASVEEDTPEKRLQKQRYMELQETLMKTFSEDKEE---CGKSSPKPKPYS--A 572  
  
 QY 578 IRPRR 582  
 DB 573 VRSNR 577  
  
 RESULT 4  
 ID Q9FHE3 PRELIMINARY; PRT; 593 AA.

Q9FHE3;  
 AC 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE REGULATORY PROTEIN NPRI-LIKE, TRANSCRIPTION FACTOR INHIBITOR I KAPPA  
 DE B-LIKE.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsiis.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RX MEDLINE=20181125; PubMed=10718197;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,  
 RT Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence  
 RT features of the regions of 3,076,755 bp covered by sixty p1 and TAC  
 RT clones.";  
 RL DNA Res. 7:31-63(2000).  
 DR EMBL; AB019224; BAB09496.1; -. 5AD457E04DC63693 CRC64;  
 SQ SEQUENCE 593 AA; 66833 MW; 5AD457E04DC63693 CRC64;  
  
 Query Match 34.3%; Score 1012.5; DB 10; Length 593;  
 Best Local Similarity 40.9%; Pred. No. 5.5e-62;  
 Matches 244; Conservative 100; Mismatches 192; Indels 61; Gaps 14;  
  
 QY 9 TNAFSDSDSASVEEGDADADADVEALRRRLSDNLAFAFRSPE-DFAFADARAVPGGGG 67  
 DB 25 SNHFSSSASNP-----VVSFLKLSNLEQLLSNSDCDY---SDAEIIVDVPVG 72  
  
 QY 68 GGDRLVHRCVLSARSFPLRGVFAARRAAAGGGGGEDGSERLERLRELLGGGEEVGVYEA 127  
 DB 73 -----VHRCILAAKSFQDLFKKKEKIS-----KTEKPKYQLREMLPYGA-----VAHEA 118  
  
 QY 128 LRLVLDYLSGRVGDLPKAAACLCVDEDCARVGHCHPAVAFMAQVLFQVFAELTNLFQ 187  
 DB 119 FLYFLSYITGRKLPFPFLEVSTCVDPVCSHDCRPAIDFVQVLMYASSVLPVELVSSQ 178  
  
 QY 188 RRLDLVDKVEVDNLLILSVANLCNCKMCLLERCLDMVVRNLDMLTLEKSLPPDVTK 247  
 DB 179 RRLCNFVETLVENVLPILWVAFNCKLT--QLLDQCIERVARSDLYRFCIEKEVPPPEVAE 236  
  
 QY 248 QIIDARLSGLTSPENKGFPPK-----HVRIRHALDSDVVELVRLMLTTEGQTNLDDA 300  
 DB 237 KIKQLR---LISPQDEETSPKISEKLERIGKILKALDSDVVELVRLMLTTEGQTNLDDA 292  
  
 QY 301 FALHYAVEHCDCKITTELLDLADLVNHNPRGYTVLHIAARRREPKEIIVSLLTKCARPA 360  
 DB 293 NGLHYSVVYSDPKVVAEILALDMDGVNRSRGYTVLHFAAMRREPSIILSIDKGNAS 352  
  
 QY 361 DVTDFGRKAVQISKRLTKOGDYFGVTEEGKPSPKDRLCIEILEQAEARRDPQLGEASVSLA 420  
 DB 353 EFTSDGSRSAVNILRLTNPKDYHTKTAKGESSKARLCIDILEREIKKNPMVLDTMCSI 412  
  
 QY 421 MAGESLRGLLYLENVALARIMFPMEARVAMDAVQDGTLEFNLCGSGANPPPE---ROR 477  
 DB 413 SMPEDLQMLLLEKRYGLAQLFFPTPEAKVAMDIGNVEGTSEF---TGLSPSSSGLTGNL 469  
  
 QY 478 TTVDLINESPFIKKEEHLARMTALSKT-----VELGKRFEPKPSNVLDKIM-----DDE 525  
 DB 470 SQVDLNETPHMQTQRLTRWALMTKGNKLLALFEGRFRFPYGVSEVLDQKYMAYETDDI 529  
  
 QY 526 TDPVSLGRDTSAB---KKRFRHDLQDVLQKAFHEDKENDRSGLSSSSSTISGAIR 579  
 DB 530 LDDFHEKSGTHERLKRMYRELKDDVQKAYSKOKESKIARSLASASSPSSSSIR 586  
  
 RESULT 5  
 ID O81848 PRELIMINARY; PRT; 601 AA.



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Db 289 SREVVKALLEGAADVNPAGPTGKTALHIAAEMVSPDMVAVLLDHDHDPNVTQVDGTP 348
      :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 370 VOISKRLTK-----QGDYFGVTEGKPSKDRLCIEILEQA-----ERRD----- 409
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 349 LDILRLTSLDFLFGAIGLTHI-EPN-KRLCLCLELVQSAALVIREEGNNNSNDNTMI 406
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 410 -POLGEASVSLAMAGESLRLLYL 433
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 407 YPRMKDEHTS-----GSSLDLSRLVYL 427
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
Q9ZVC2 PRELIMINARY; PRT; 491 AA.
AC Q9ZVC2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE F13H10.8 PROTEIN.
GN F13H10.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RA "Arabidopsis thaliana chromosome II BAC F13H10 genomic sequence.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005662; AAC78536.1; -
DR InterPro; IPR000210; -
DR InterPro; IPR002110; -
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00651; BTB; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50097; BTB; 1.
DR SMART; SM00248; ANK; 1.
SQ SEQUENCE 491 AA; 54001 MW; F2E8A7133B591776 CRC64;

Query Match 14.3%; Score 421; DB 10; Length 491;
Best Local Similarity 29.2%; Pred. No. 3.6e-21;
Matches 135; Conservative 72; Mismatches 170; Indels 86; Gaps 15;

Qy 32 EALRLRLS---DNLAFAFRSPEDFAFLADARIAVPGGGGGDLRHVRHCVLSARSFPLRGV 88
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 ESLSRLSLDFNLINGQAFSDVTSVEGR-----VHAHRCILARSLEFFKRF 54
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 89 FARRAAAAGGGGEGSGERLELRLGGGGEV-----EVGYEARLRLVL 132
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 55 FC-----GTDSPQPVGTIDPTQHGSPVSPASPTRGSTAGIIPVNSVGYEVFLLLL 104
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 133 DYLSGRVGDLP---KAACLVDDECAHVGCHPAVAFMAQVFASTFOVLETLNLFQR 189
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 QFLYSQGVSIPOKHEPRNCGERCWHTHCSAAVDLADLTAAASRYFVEQALLTKQK 164
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 190 LLDVLDKVBDVNDLLITSLVANLCNCKMLERCLDMVVRSLDMLTLEKSLPPDVVVKI 249
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 165 LASMVEKASIDSPHNNHHDLSSVAQDLEQKIRRMRLDSSDVELYKLVMGEGNL 282
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 250 IDARLSLGL-----ISPEN-----KGFNKHVRIHRLSDSDVELYMLLTGQTNL 297
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 EELRLKSSSTARSLPHNNHHDLSSVAQDLEQKIRRMRLDSSDVELYKLVMGEGNL 282
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 298 DDAFALHYAVEHCDSKITTELLDLALADVNH--RNPFGYTVLHIAARRRPKPIVSLITKG 356
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 DESLALHYAVESCSREVVKALLEGAADVNPAGPTGKTALHIAAEMVSPDMVAVLLDHH 342
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Qy 357 ARPADVTFDGRKAVOISKRLTK-----QGDYFGVTEGKPSKDRLCIEILEQA----- 405
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 343 ADPNVTVGGITPLDLRLTSLDFLFGAIGLTHI-EPN-KRLCLCLELVQSAAMVISRE 400
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 406 -----ERRD-----POLGEASVSLAMAG--ESLRGLLYL 433
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 401 EGNNSNNONNDNTGIYPHMNEHNSGSGSGNNLDSRLVYL 443
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RESULT 8
Q9VXM6 PRELIMINARY; PRT; 993 AA.
AC Q9VXM6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CG16952 PROTEIN.
GN CG16952.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.D.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.N., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wessarman D.A., Weisscock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; -
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003500; AAF48532.1; -
DR FlyBase; FBgn0030701; CG16952.
DR InterPro; IPR000210; -
DR Pfam; PF00651; BTB; 1.
DR PROSITE; PS50097; BTB; 2.
DR SMART; SM00225; BTB; 1.
SQ SEQUENCE 993 AA; 108604 MW; B62CF6E625BAD788 CRC64;

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Query Match	5.1%;	Score 151.5;	DB 5;	Length 993;
Best Local Similarity	21.3%;	Pred. No. 0.045;		
Matches	142;	Conservative	86;	Mismatches 243;
				Indels 195;
				Gaps
Qy	1	MEPPTSHVTNAFSDSDSASVEEGDA--DADADVEALRRSLDNLAARSPDEDAFL---	54	
Db	209	LELPTSPIDVQLFESSLLRYLYTGDLCPHPDNTDITLLRQLGDKFGTPNPLEHDLRYLLET	268	
Qy	55	---ADARIAVPGGGG-----GG-----DURVHRCVLSARSPELGRGVARRAA	95	
Db	269	GDYADAALVFTADGSDNDYLRODSGTSEYGFPRPKIELPCHKAILSARSPEFRNLIAARTR-	327	
Qy	96	AAGGGEDGGER--LELRELLGGGEEVEGYEALRLVDLYLSRGVGDLPKAAACLCDV	152	
Db	328	---NMDEYVERSLHVPTRIVL---DETPIPKRYARVILQAILDSV--DLSLI-----	372	
Qy	153	EDCAHVGCHPAVAFMAQVLFAASTFOV-----AELNLFQ---RRL--LDVLDKVEVDNLIL	204	
Db	373	--LRVGSGTSAAGSLGEVHALTWGRVPTTLEEAMELYQIGREFELDILAQCCEDLIILE	430	
Qy	205	ILSVANL-----C-----NKSMCKLLERCIDMWVRSNLDMITLEKSLPPDVVK-	247	
Db	431	WLSIETLPTVLKWCQCOPHGSAAVFRQACQYLREEF--AAVSSPVLRLDKSKLIHILHS	488	
Qy	248	-----QIIDARLSLG---LISPENKFPNKHVRH-----RALDSDDELVELVRL	289	
Db	489	NFOASELVLQAVLKWGEQELTRMEDREPNNLSHTAHSAVKRGVKKRDLSDIEL-----	544	
Qy	290	LTEGOTNLDDAFALHYAVECHDSKITTELLDLALADVNRHNPGRYVNLHIAARRRPEKII	349	
Db	545	-----REILSELLPYRMD--HVLPHCEVLQCAIRG-----L	576	
Qy	350	VSLLTGARGADVTFDGRKAVQISKRL---TKQG-----DYGVTVEEGKPSKDL	397	
Db	577	VS-----TPPSHMTGDDRENLRINAWIRGGKNOGLYVRPRLEMPYF---EEVKALLEDRM	628	
Qy	398	C-----TEILEQAE-RDPOLGASYSLAMAGESLGRLLYLENRVALARIMPMEARVA	451	
Db	629	SSSHQVLEMMRRRCRHPDPDPTLYNVSHMNSKANSDLSTVENR-----	673	
Qy	452	MDIAQVDGTLFENLGANPPPERQRTVTDLNSPFIKMEEHLMARMTALSKTVELGKRF	511	
Db	674	---STDGNVDILYGAAVIPPPDNQTLA-----MRKREHLRQS-----	709	
Qy	512	PRCSNVLDKIMDDTDPVSLGROTSABKRRFH---DLQDVLOKAFHEDKEENDRSGLS	568	
Db	710	PMCQRALLPLSSKSE---IDRQIRLVVREFPNLDEVSDDLLESALQTPNGRNE-SHAEE	765	
Qy	569	SSSSTS	574	
Db	766	TSASTS	771	

## 9 RESULT

Q99407	Q99407	PRELIMINARY;	PRT; 1856 AA.
ID	AC	Q99407;	
DT	DT	01-MAY-1997	(TREMBLrel. 03, Created)
DT	DT	01-MAY-1997	(TREMBLrel. 03, Last sequence update)
DT	DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)
DE	DE	ANKYRIN.	
GN	GN	ANK1.	
OS	OS	Homo sapiens (Human).	
OC	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	OX	NCBI_Taxid=9606;	
		[1]	
RN	RN	SEQUENCE FROM N.A.	
RP	RP	Forgot B.G., Tse W.T., Gallagher P.G., Scarpa A.L., Lux S.E.;	
RA	RA	Submitted (Feb-1996) to the EMBL/GenBank/DBJ databases.	
RL	RL		
DR	DR	EMBL; U50133; AAB47805.1; -	
DR	DR	EMBL; U50092; AAB47805.1; JOINED.	

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Query Match      4.88; Score 143; DB 4; Length 1856;
Best Local Similarity 23.99; Pred. No. 0.43;
Matches 76; Conservative 37; Mismatches 107; Indels 98; Gaps 12;

QY 271 VRRTHRALDSDVELVRMLLT-----EGOTNLDDAF----- 301
      | | | | | : | : | : | | | | | | | | | | | |
Db 603 VTFPLHAAQEHAERWALLLSKQANGNLGKSGLTPLHLVQAEGHVPADVLIKHGVMD 662

QY 302 -----ALHYAVEHCDSKTITTELLDALADVNRHNPGRYTVLHIAARRREPKTIIVSLL 353
      | | | : | : | | | : | | | : | | | : | | | : | |
Db 663 ATTRMGVYTPLHVASHYGNIKLVKFLQ--HQADVNAKTKLGYSPLHQAAQOQGTDIVTLLL 721

QY 354 TKGARPADVTFDGRKAVQISKRLTKQGDYFGVTEEGK-----PSPKDRLCI---- 399
      | | | | | : | | | | | : | | | : | | | : | | | : | |
Db 722 KNGASPNVSDSGTTPLAIAKRL---GYISYTDVLKVTDETSEFLVSKDRHNSFPETV 777

QY 400 -EILEQAEERDPQGEASVSLMAGESLURGLLYLENRVALARIMFPPEARVMDIAQVD 458
      | | | : | : | | | : | | | : | | | : | | | : | |
Db 778 DEILDVSE-----DEGTAHTITMGEEL-----TSFKAEKRSRSDVEEK 816

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Query Match	4.8%;	Score 143;	DB 4;	Length 1856
Best Local Similarity	23.9%;	Pred. No. 0.43;		

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QY 459 GTLEFNLSGANPPPRQRTTVDLNEPIMKEELHARMTALSKTVLCKRFFPRCSNVL 518
DB 817 ELUDF-----VPLKQV-----ESPAIRP-----CAMPETVIRSEOEQASKEY 859
QY 519 DKIMDETPVSLGRDTS 536
DB 860 D---EDSLIPSPATETS 874

RESULT 10
ID Q9U3S0 PRELIMINARY; PRT; 597 AA.
AC Q9U3S0;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)
DT 01-MAY-2001 (TREMREL. 16, Last annotation update)
DE C04F12.3 PROTEIN.
GN C04F12.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z81461; CAB62796.1; -.
DR HSSP; P42773; 1IIB.
DR InterPro; IPR000488; -.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR SMART; SM00248; ANK; 1.
SQ SEQUENCE 597 AA; 66421 MW; CD271B6B4CF25A35 CRC64;

Query Match 4.8%; Score 140.5; DB 5; Length 597;
Best Local Similarity 20.1%; Pred. No. 0.12;
Matches 107; Conservative 92; Mismatches 202; Indels 131; Gaps 23;

QY 73 VHCRLVLSRSPFLRGVFAARRAA-----AAGGGEDGSERLERLRLGGGEEVEGYEA 127
DB 32 IHKSSQHRRLFIDDIISTEASAGDRWATCAGAGATELTIHFLL---GDQFEESAIDV 88
QY 128 LR---LVLDLYLSGRVGLPKAACLCVDECAHVGHCPAVAFMAQVLFAASTFQVAELTN 184
DB 89 VRKSLVMTVPSS-----LKVDS-----LEVELRESTNDNVTTFISF 126
QY 185 LFQRLLDVLDKVEV---DNLLILSVANLCKNSCKMLLERCLDMVVRNLDMIT----- 236
DB 127 KYLPRKIQRSHQTEISLNFNLLEFAT-----NGDTISLLQPFVAQISKQDIEGTVFHYA 181
QY 237 -----LEKSLPPDVVIQIIDARLSLGLISPENKGFNKHVRRTHRALDSDDEL 285
DB 182 ANKQSFSLKLLSVIPDKNKEVINQVTHGLTA-----LHVAIRTGDDPA 228
QY 286 VRMLTLEG-QTNLDD---AFALHYAVEHCDKITTLELLDALA---DVNHRNPRGYTVLH 338
DB 229 VHYLMNHGAKIDISDNHGSTALHYGLDAYNESIFKILEPSCQRQFDVQNLSEGAPIH 288
QY 339 IAARRREPKIIVSLTKGAPADVTF-DGRKAVQISKRLTKQGDYFGVTEEGKPSPKDL 397
DB 289 VAVRRLKLSLIEMLIEAGAL---IDFLDTEKRRNALMHAEMNDFETI-----QL 335
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QY 398 CIEILLEQARRDPOLGEASVSLAMAGESLRGLLYLENVALRIMPFPMEARVAMDIQV 457
DB 336 LVERGSGTNIED-ESGETALSLAVKNVNPVYIGLLDNGADPNR-----ONSKGICLADS 389
QY 458 DGTLEFNLSGANPP-PRQRTTVD-----LNESPFT-----MKE 491
DB 390 EDSVIONINGDRPELPKKEAFGVNDLAISRPLFCGRSHPDQAPGEEGRHVVRKRSR 449
QY 492 EHL-ARMTALSKTVLKGKRRFFPCSNVLDKIMDDETPVSLGRDTSAAEKRR 542
DB 450 EILNDAQTLLETDSMA-----PRVSRISTSESEDEQP---GPSTSGTTRR 494

RESULT 11
ID Q9FRM5 PRELIMINARY; PRT; 265 AA.
AC Q9FRM5;
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)
DE PUTATIVE ANKYRIN PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae;
OC Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNba0056G17 genomic sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC018727; AAG46181.1; -.
SQ SEQUENCE 265 AA; 27930 MW; BFCA48939F8B0200 CRC64;

Query Match 4.6%; Score 135.5; DB 10; Length 265;
Best Local Similarity 19.8%; Pred. No. 0.084;
Matches 75; Conservative 37; Mismatches 88; Indels 179; Gaps 11;

QY 63 GGGGGGDLRVHRCVLSARSFPLRGVFAARRAAAGGGEDGSERLERLRLGGGEEVE 122
DB 6 GGGGGGG-----GGRGGRGR-----GGGEEDD 29
QY 123 VGYEALRLVDLYL-SGRVGLPKAACLCVDECAHVGHCPAVAFMAQVLFAASTFQVAE 181
DB 30 L-----HLHKAARSGDLAAESLC----- 48
QY 182 LTNLFORLLVDKVEVDNLLILSVANLCKNSCKMLLERCLDMVVRNLDMITLEKSL 241
DB 49 -----EANPLAL-----NSRDLRSRTP----- 66
QY 242 PPDVIQIIDARLSLGLISPENKGFNKHVRRTHRALDSDDELVRMLLTE-----GOTNL 297
DB 67 -----HLAAGHVELVKCLCKHKHADVAAM 93
QY 298 DDAFALHYAVEHCDKITTLELLDALADVNHNRNPRGYTVLHIAARRREPKIIVSLTKGA 357
DB 94 DDTAAIHFAQSQGHVVRRELL-ASGASVAKNRKGFTALHFASQNSHLELVLYLVKGA 152
QY 358 RADVTDFGRKAVQISKR-----LTKQGDYFGVTEEGKPSPKDLRCLILEQ 404
DB 153 DIAAKTKGQGTALHVAEKDDVRDLFKECEQSLKKGEL-----PSEKKDSDSVSTIAE 204
QY 405 AERRDPQLGEASVSLAMAG 423
DB 205 KPDDKSSGEATKDEDEAG 223
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348 SHKSLANPGLMKEEPTKPGIAKKENGIDI 376

348 SHKSLANPGLMKEEPTKPGIAKKENGIDI 376

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RESULT 14
Q9H1Q1 PRELIMINARY: PRT: 1710 AA.
ID Q9H1Q1
AC Q9H1Q1
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE BAI45E8.1 (KTA1074).
GN BAI45E8.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL162272; CAC19649.1;
SQ SEQUENCE 1710 AA; 196410 MW; 01CBF9BAD894872 CRC64;

Query Match 4.6%; Score 135; DB 4; Length 1710;
Best Local Similarity 19.4%; Pred. No. 1.4;
Matches 99; Conservative 68; Mismatches 176; Indels 166; Gaps 17;

QY 87 GVFARRAAAGGGGDSERLELLGGGEEVEVGEALRLVLDYLSRGVGDLPKA 146
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 GSFARRORSSAGGGGEGE-----GAYSQPGYHVR----- 43
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 147 ACLCDEDCARHVGCHPAVAFMAQVLAFASTFOVAELTNLFQRRLDVLDKVEVDNLLIL 206
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 44 -----DRD-----LCKIHKASAGNVAKVQILLKRLKGLNDRDKMRTALHL 86
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 207 SVANLCNCKMKLLERCLDMVYRSLDMITLEKSLPPDVVIQIDARLSGLISPENKGF 266
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 87 ACAN-----GHPEVTVLLVDRKCKQLNVCNDENR--- 114
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 267 PNKHVRRTHRALSDSDVELVRLMTEG-QTNLDDAF-----ALHYAVEHCDSKITTELLDLA 322
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 -----TALMKAVQCEERKATILLEGADPNLADVHGNTALHYAVINEDISVATKLL-LY 168
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 323 LADVNRNPRGTVLHIAARRREPILVSLFLKGPADVTFDGRKAVQISRLTKQGDY 382
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 169 DANIEAKNKDDLTPLLAVSGKKQVVELIKKA----- 203
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 383 FGVTEGRSPKDRLCIELEQARRDPOLGEASVSLAMAGESLRGLLYLENRVVALARI 442
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 204 -NVNAVDKLESSHLITSEYKE--ERIPKHSQNSNSVDESSEDSLSRL----- 248
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 443 MFPMEARVAMDTA-----QVDTGLEFNLGSGANPPPERQRTVDLNSPFTMKEEHLARMTA 499
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 249 -----SGKPGVDDSWPTSDDEDLNFTKNVPKPSLAKLMTA-----SQQSRKNLEA 294
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 500 LSKTVELGKR--FFPRCSNVLDKIMDETDPVSLGRDTSAEKRRKF-----HDLQDVLOKA 553
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 295 TGTGTVRTGRTLFEDRDSQSEVVEVSESLPTTSI-----KVQCFSHPTYSPLLPKP 347
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 554 FHED-----KEENDRSGLSSSSSSTSI 575
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 348 SHKSLANPGLMKKEPTKPGIAKKENGIDI 376
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
Q9VT60 PRELIMINARY: PRT: 877 AA.
ID Q9VT60
AC Q9VT60
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE CG6718 PROTEIN.
GN CG6718.

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OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liao P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J., Yang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Rao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003550; AAF50194.1; -.
DR HSSP: P25963; 1IKN.
DR FlyBase: FBgn0036053; CG6718.
DR InterPro: IPR002110; -.
DR InterPro: IPR002641; -.
DR Pfam: PF00203; ank; 5.
DR Pfam: PF01734; Patatin; 1.
DR PROSITE: PS50088; ANK_REPEAT; 3.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR SMART: SM00248; ANK; 1.
SQ SEQUENCE 877 AA; 96862 MW; C9DC2CD6C282869B CRC64;

Query Match 4.5%; Score 133.5; DB 5; Length 877;
Best Local Similarity 20.2%; Pred. No. 0.66;
Matches 92; Conservative 63; Mismatches 167; Indels 133; Gaps 19;

QY 189 RLDDVLDKVEVDNLLILLSVANLCNCKMKLLERCLDMVYRSLDMITLEKSLPP 243
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 141 KMLQCVQDAATAATLMSPFOLA--IKQGHMEVYKALLPLSKLEHLIDINSVFEHYAATTK 198
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 244 DVIKQIIDARLSGLISPENKGFNKHVRIRHRLDSDSDVELVRLMTEG----- 293
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 199 EITNLIID-KSTVNLNHLNSDGYTPLHV-----ACLADKPNVYKALLAGANVNLAKDI 252
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

QY 294 -----QTNLDDAFA-----LHYAVEHCDSKITTELLDALADVNH 328
| | | | : | | | | | | | | | | | | | | | | | | | | | | | |

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2001, 17:12:38 ; Search time 22.27 Seconds  
(without alignments)  
1584.336 Million cell updates/sec

Title: US-09-294-539-4  
Perfect score: 2952  
Sequence: 1 MEPTSHVTNAFSDSDASV.....RSLSSSSSTSGAIRPRR 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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  - 21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*
  - 22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2952	100.0	582	22	Rice NPR1 homologue
2	2910	98.6	578	21	Rice putative nega
3	1737	58.8	576	21	L. esculentum NIM1
4	1672.5	56.7	588	19	Nicotiana glutinos
5	1672.5	56.7	588	21	N. tabacum NIM1 ho
6	1629	55.2	604	21	B. vulgaris NIM1 h
7	1285	43.5	593	21	Arabidopsis thalia
8	1276	43.2	593	19	A. thaliana NIM-1
9	1276	43.2	593	19	Arabidopsis thalia
10	1276	43.2	593	19	Arabidopsis thalia
11	1272	43.1	593	19	A. thaliana non-in

12	1270	43.0	593	19	AAW64436	A. thaliana varian
13	1270	43.0	593	19	AAW61983	Non-inducible immu
14	1222.5	41.4	579	21	AAAB27303	B. napus NIM1 homo
15	1213.5	41.1	600	21	AAAB27307	A. thaliana NIM1 h
16	1213.5	41.1	601	21	AAAB27328	A. thaliana NIM1 h
17	1188.5	40.3	521	19	AAW64438	A. thaliana C-term
18	1188.5	40.3	521	19	AAW61985	Non-inducible immu
19	1134	38.4	469	19	AAW64437	A. thaliana N-term
20	1134	38.4	469	19	AAW61984	Non-inducible immu
21	1087	36.8	621	21	AAAB36271	Maize NPR1 transla
22	1087	36.8	621	21	AAAB36272	Maize NPR1 transla
23	1060.5	35.9	591	21	AAAB27325	H. annuus NIM1 homo
24	1052.5	35.7	397	19	AAW64439	A. thaliana C- and
25	1052.5	35.7	397	19	AAW61986	Non-inducible immu
26	1045.5	35.4	609	22	AAAB48088	Wheat Nph2-2 prote
27	1045	35.4	607	22	AAAB48087	Wheat Nph2-1 prote
28	1043	35.3	427	21	AAAG17534	Arabidopsis thalia
29	1031	34.9	586	21	AAAB27304	A. thaliana NIM1 h
30	1031	34.9	586	21	AAAG1887	Arabidopsis thalia
31	1009	34.2	574	21	AAAB27327	A. thaliana NIM1 h
32	995	33.7	475	22	AAAB48086	Rice Nphl protein.
33	987	33.4	455	22	AAAB09876	Rice putative nega
34	971.5	32.9	601	21	AAAB27306	A. thaliana NIM1 h
35	946.5	32.1	479	21	AAAG1888	Arabidopsis thalia
36	904	30.6	377	21	AAAG17535	Arabidopsis thalia
37	844.5	28.6	409	22	AAAB48093	Protein encoded by
38	842.5	28.5	425	21	AAAG1889	Arabidopsis thalia
39	825	27.9	217	21	AAAB27316	S. tuberosum NIM1
40	823	27.9	219	21	AAAB27308	N. tabacum NIM1 ho
41	782.5	26.5	381	22	AAAB48091	Putative protein e
42	751	25.4	261	19	AAW64440	A. thaliana NIM-1
43	751	25.4	261	19	AAW61987	Non-inducible immu
44	739	25.0	325	21	AAAB09874	Corn negatively ph
45	678	23.0	369	21	AAAB27329	N. tabacum NIM1 ho

## ALIGNMENTS

### RESULT 1

AAAB29750  
ID AAB29750 standard; Protein; 582 AA.

XX AC AAB29750;

XX DT 28-FEB-2001 (first entry)

XX DE Rice NPR1 homologue 1 (NIM1), SEQ ID NO:4.

XX KW Rice; NIM1; NPR1 homologue 1; PNI interactor; SAR; bzIP protein;  
KW systemic acquired resistance; yeast two-hybrid system; transgenic plant;  
KW pathogen resistance; virus; bacterium; nematode; fungus; insect.

XX OS Oryza sativa.

XX PN WO200063417-A2.

XX PD 26-OCT-2000.

XX PF 06-APR-2000; 2000WO-US09060.

XX PR 19-APR-1999; 99US-0294539.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Chern MS, Ronald P;

XX DR WPI; 2001-090867/10.

XX DR N-PSDB; AAC81457.

XX PT Novel nucleic acid construct for enhancing pathogen resistance, encodes  
PT rice proline rich NPR1 interactor proteins, polypeptides interacting  
PT with PNI or MNI, and bzIP protein interacting with Arabidopsis NPR1

xx The invention relates to rice proteins (AAB29749-B29757) and the  
ps nucleotides encoding the proteins (AAC81456-C81464), which are involved  
cc in the induction of systemic acquired resistance (SAR), a general plant  
cc resistance response that can be induced during a local infection by an  
cc avirulent pathogen. A rice cDNA library was screened using the yeast two  
cc hybrid system with Arabidopsis NPR1 cDNA as bait, and the rice proteins  
cc PNI (proline rich NPR1 interactor; AAB29749) and MNI (AAB29758) were  
cc identified as interacting with Arabidopsis NPR1. The rice cDNA library  
cc was then rescreened using rice PNI cDNA or rice MNI cDNA as bait. Rice  
cc NH1 and NH2 (NPR homologues 1 and 2; AAB29750, AAB29751), nucleolin-like  
cc protein (AAB29752), PREG-like protein (AAB29753), and a protein with no  
cc known homology (AAB29754) were identified as interacting with PNI  
cc protein, and rice GRL1 and GRL2 (glutaredoxin homologues 1 and 2;  
cc AAB29755, AAB29756) and rice MAP1A (a protein with homology to rat  
cc microtubule-associated protein; AAB29757) were found to interact with  
cc rice MNI protein. The invention additionally encompasses transgenic  
cc plants comprising an expression cassette encoding a protein of the  
cc invention, and a method for enhancing resistance to pathogens in a plant  
cc by introducing the expression cassette into the plant, and selecting the  
cc plant with enhanced resistance. The rice SAR-associated nucleic acids and  
cc proteins are useful for enhancing plant resistance to pathogens such as  
cc viruses, bacteria, nematodes, fungi or insects. The present sequence  
cc represents rice MNI.  
xx  
SQ Sequence 582 AA;

Query Match 100.0%; Score 2952; DB 22; Length 582;  
Best Local Similarity 100.0%; Pred. No. 7.6e-277;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEPTSHVTNFAFSDSASVEEGDADADADVEALRRLLSDNLAARSPEDFAFLADARIA 60  
Db 1 meptshvtnafdsdsasveegdadadadvealrrlsdnlaaafsrpedfafladaria 60  
Qy 61 VPGGGGGDLVRHRCVLSARSPLRGVFAARRAAAAGGGGDSERLELRELLGGGEE 120  
Db 61 vpgggggdvlrvhrcvlsarsplrgvfarraaaaaggggdserlelrellgggee 120  
Qy 121 VEVGYEARLRLVLDLYSGRVGDLPKAACLCVDEDCAHVGHCPAVAFMAQVLFPAASTFQVA 180  
Db 121 vevgyearlrlvldlysgrvgdplkaacclvdedcahvghcpavafmaqvlfaastfqa 180  
Qy 181 ELTNLFQRLLDLVDKVEVDNLLILSVANLCNCKMLLERCLDMVRSNLDMLTLEKS 240  
Db 181 eltnlfqrrlldvdkvevdnllilsvanlcnckmllercldmvrnsldmltleks 240  
Qy 241 LPPDVIKQIDARLSGLISPENKGFNPKHVRRIHRAALSDDDVELVRLMLTEGQTNLDDA 300  
Db 241 lppdvikqidarlsglispenkgfnpkhvrrihraalsddvelvrlmltegqtnldda 300  
Qy 301 FALHYAVEHCDSKITTLELDDALADVNRHNRPGYTVLHIAARRREPKIIVSLTLKGARPA 360  
Db 301 fallyavehcdskittellldaladvnrhnrpgyvtvlhiaarrrepkiivsltlkgarpa 360  
Qy 361 DVTFGDKRAVOISKRLTKQGYFGVTEGKPSKDKRLCIELEOARERDPOLGEASVSLA 420  
Db 361 dvtfgdkravoisrkrltkogyfgvteegkpskdkrlcieleoaerdpolgeasvsla 420  
Qy 421 MAGESLRGRLLYLENRVALARIMFMEARVAMDIQAQVDTGLEFNLGSGANPPPQRQRTTV 480  
Db 421 mageslrgrrllylenrvalarimfmearvamdiqaqvdtglefnlgsganppperqrttv 480  
Qy 481 DLNESPFTMKEEHLARMTALSKTVELGKRFPNCRSNVLDMKIMDETDPVSLGRDTSABKR 540  
Db 481 dlnespftmkeehlarmtalstvelgkrfpncrsnvlldmldetdpvslgrdtsabkr 540  
Qy 541 KRFHDLQDLQKAFHEDKEENDRSGLSSSSSSTSTGALRRPR 582  
Db 541 krfhdlqdlqkafhedkeendrsglssssststgairrr 582

RESULT 2

AAB09875  
ID AAB09875 standard; Protein; 578 AA.  
XX  
AC AAB09875;  
XX  
DT 12-OCT-2000 (first entry)  
XX  
DE Rice putative negatively phytochrome regulated 1 (NPR1) gene product #1.  
XX  
KW Rice; negatively phytochrome regulated 1 gene; NPR1;  
KW systemic acquired resistance; gene mapping; transgenic plant.  
XX  
OS Oryza sativa.  
XX  
PN WO200028036-A2.  
XX  
PD 18-MAY-2000.  
XX  
PF 04-NOV-1999; 99MO-US25953.  
XX  
PR 05-NOV-1998; 98US-0107242.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Famodu OO, Fang Y, Liu Z, Miao G, Odell JT;  
XX  
DR WPI; 2000-451636/39.  
XX  
DR N-PSDB; AAA61047.  
XX  
PT Isolated nucleic acid fragments encoding an NPR1 gene which can be used  
PT to transform plants and provide disease resistance  
XX  
PS Claim 1; Page 29; 35pp; English.  
XX  
CC The present sequence is the product of a putative version of the corn  
CC negatively phytochrome regulated 1 (NPR1) gene. Its coding sequence was  
CC isolated by screening a leaf cDNA library for those sequences  
CC which were similar to the NPR1 gene from Arabidopsis thaliana. This  
CC protein is involved in systemic acquired resistance and its gene can be  
CC used to create transgenic plants which are protected from pathogens. It  
CC can also be used to find homologous sequences in other plants which have  
CC a similar effect.  
XX  
SQ Sequence 578 AA;

Query Match 98.6%; Score 2910; DB 21; Length 578;  
Best Local Similarity 99.5%; Pred. No. 8.7e-273;  
Matches 575; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 5 TSHVTNFAFSDSASVEEGDADADADVEALRRLLSDNLAARSPEDFAFLADARIAVPGG 64  
Db 1 tshvtnafdsdsasveegdadadadvealrrlsdnlaaafsrpedfafladariavpvg 60  
Qy 65 GGGGGDLVRHRCVLSARSPLRGVFAARRAAAAGGGGDSERLELRELLGGGEEVEVG 124  
Db 61 gggggdvlrvhrcvlsarsplrgvfarraaaaaggggdserlelrellgggeeveg 120  
Qy 125 YEALRLVLDLYSGRVGDLPKAACLCVDEDCAHVGHCPAVAFMAQVLFPAASTFQVAELTN 184  
Db 121 yealrlvldlysgrvgdplkaacclvdedcahvghcpavafmaqvlfaastfqvaelt 180  
Qy 185 LFORRLDLVDKVEVDNLLILSVANLCNCKMLLERCLDMVRSNLDMLTLEKSLPPD 244  
Db 181 lforrlldvdkvevdnllilsvanlcnckmllercldmvrnsldmltlekslppd 240  
Qy 245 VIKQIDARLSGLISPENKGFNPKHVRRIHRAALSDDDVELVRLMLTEGQTNLDDAFALH 304  
Db 241 vikqidarlsglispenkgfnpkhvrrihraalsddvelvrlmltegqtnldafalh 300



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PR 10-JAN-1997; 97US-0035166.
XX (GEO) GEN HOSPITAL CORP.
PA (UYDU-) UNIV DUKE.
XX Ausubel FM, Cao H, Dong X, Glazebrook J;
XX WPI; 1998-159458/14.
XX N-PSDB; AAV16852.
XX New isolated plant acquired resistance polypeptide gene - useful
PT for, e.g. producing plants with increased resistance to pathogens
PT such as bacteria
XX Claim 26; Fig 7; 127pp; English.
XX The sequence is that of encoded by a homologue of the acquired
CC resistance gene NPK1. Transgenic cells which produce such a
CC protein are useful in the production of plants having
CC an increased level of resistance against disease caused
CC by plant pathogens, e.g. bacteria, mycoplasmas, fungi, insects,
CC nematodes, viruses, and viroids.
XX Sequence 588 AA;

Query Match 56.7%; Score 1672.5; DB 19; Length 588;
Best Local Similarity 56.8%; Pred. No. 5.4e-153;
Matches 336; Conservative 102; Mismatches 119; Indels 35; Gaps 8;

Qy 11 AFSDSDSASVEE-----GDADADAEALRLRLSDNLAFAF-RSPEDFAFLAD 56
Db 7 afdsndisgssiccggtteffspetspaetsikrlsetiesifdaslpedyfad 66

Qy 57 ARIAPVGGGGGDLRHVRCVLSARSPLRGVFAARRAAAGGGGEGSERLELRELLGG 116
Db 67 akllv---sgpkelpvhrclarspffknlf-----gkknsskvelkvm-- 113

Qy 117 GGEVEVEYALRLVLYSGRGVGLPKAACLCVDECAHVGHCHPAVAFNAQVLF 176
Db 114 --kehevsydavmsvlaylysgkvrpskdvccvndcshvacrpavafivevlytsft 171

Qy 177 FOVAELTNLFORLLDVKVEVDNLLILSVANLCKNSCKMLERCLDMVVRNLDMIT 236
Db 172 fqiselvdkfqrhlldlkdtaadvmvlsvanicgkacerllsscieiivksnvdit 231

Qy 237 LEKSLPPDVIKQIIDARLSGLISPENKGFNKHVRTRHRALDDSDVVELVRLMTEGOTN 296
Db 232 ldkalpdhivkqitdsraelglqpesngfokhvkrihraldsdvvelqllreghttt 291

Qy 297 LDDAFALHYAVEHCDSKTTTELDDALADVNRNPRGTYVLHIAARRRPEKIIIVSLTKG 356
Db 292 lddayalhavyaycdakttaelldlaladinhqnsrgyvtlvhvaamrkepkivvslitkg 351

Qy 357 ARPADVTEDGKAVQISKRLTKQDYGVTTEGKPSKDRLCIELEQAEERDPQLGEAS 416
Db 352 arpsdltsdgrkaiqrklrlvdfkspeegksasndrlciellegaeerrdpllgeas 411

Qy 417 VSLAMAGESLRLGLYLENRVALARIMPEARVAMDAQVDGTLFNLGSGANPPPERQ 476
Db 412 vslmagadglrmklllylenrvglakllfpmeakvamdlaqvgdtsefplagikgmanaq 471

Qy 477 RTVDNLNESPFTIMKEELHARMTALSKTVELGKRFPPRCNSVLDKIM--DDFTDPSVLRD 534
Db 472 rttvdnlneapfkkeehlnrlalsrtvelgkrtffprcsevlnkimdaddlseiyngnd 531

Qy 535 TSAE---KRRFPHLDQVQLQAFHDEKRENDR-SGLSSSSSSSTSGATRRPR 582
Db 532 taerqikqymelqelkftaedkeydktnnissscsstsgkvgdkpnk 583

RESULT 5
AAB27301

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ID AAB27301 standard; Protein; 588 AA.
XX AAB27301;
XX AC AAB27301;
XX DT 25-JAN-2001 (first entry)
XX DE N. tabacum NIM1 homologue SEQ ID NO: 2.
XX KW Systemic acquired resistance; SAR; signal transduction cascade;
XX KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
XX OS Nicotiana tabacum.
XX PN WO200053762-A2.
XX PD 14-SEP-2000.
XX PF 07-MAR-2000; 2000WO-EP01978.
XX PR 09-MAR-1999; 99US-0265149.
XX PA (NOVS) NOVARTIS AG.
XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX PI Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
XX DR WPI; 2000-594322/56.
XX DR N-PSDB; AAS97190.
XX PT Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are
PT homologues of Arabidopsis NIM1 gene -
XX Claim 1; Page 70-72; 152pp; English.
XX The present invention is concerned with the isolation of NIM1 homologues
XX and their coding sequences from Arabidopsis thaliana, Brassica napus,
XX Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
XX annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
XX signal transduction cascade leading to systemic acquired resistance (SAR)
XX in plants. This gives the plants an increased resistance to disease. The
XX protein and gene can be used to produce transgenic plants resistant to
XX diseases caused by viruses, such as tobacco or cucumber mosaic virus,
XX ringpot virus, pelargonium leaf curl virus, red clover mottle virus,
XX tomato bushy stunt virus, fungi, including Phytophthora parasitica and
XX Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
XX tabaci, insects, including aphids and lepidoptera and nematodes such as
XX Meloidogyne incognita. In particular they can be used against disease
XX organisms of maize.
XX Sequence 588 AA;

Query Match 56.7%; Score 1672.5; DB 21; Length 588;
Best Local Similarity 56.8%; Pred. No. 5.4e-153;
Matches 336; Conservative 102; Mismatches 119; Indels 35; Gaps 8;

Qy 11 AFSDSDSASVEE-----GDADADAEALRLRLSDNLAFAF-RSPEDFAFLAD 56
Db 7 afdsndisgssiccggtteffspetspaetsikrlsetiesifdaslpedyfad 66

Qy 57 ARIAPVGGGGGDLRHVRCVLSARSPLRGVFAARRAAAGGGGEGSERLELRELLGG 116
Db 67 akllv---sgpkelpvhrclarspffknlf-----gkknsskvelkvm-- 113

Qy 117 GGEVEVEYALRLVLYSGRGVGLPKAACLCVDECAHVGHCHPAVAFNAQVLF 176
Db 114 --kehevsydavmsvlaylysgkvrpskdvccvndcshvacrpavafivevlytsft 171

Qy 177 FOVAELTNLFORLLDVKVEVDNLLILSVANLCKNSCKMLERCLDMVVRNLDMIT 236
Db 172 fqiselvdkfqrhlldlkdtaadvmvlsvanicgkacerllsscieiivksnvdit 231

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QY 237 LEKSLPPDVIKOIIDARLSGLISPENKGFNPKHVRIHRLDSDVVELVRLMLTEGOTN 296  
 Db 232 ldkaliphdivkqitdsraeigqpgesngfpdkhvkrihraldsddveligmlregntt 291  
 QY 297 LDDAFALHYAVEHCHDSKITTELDDALADVNHRNPRGYTVLHIAARRREPKIIVSLLRKG 356  
 Db 292 lddayalhyavaycdaktaeildaladinhqnrgyvtvlhvaamrkepkivvslitkg 351  
 QY 357 ARPADVTGDKAVOISKRLTKQGYFGVTEEGKSPKDRLCIEILEQAERDPOLGEAS 416  
 Db 352 arpsdltsgdgrkalqakrltrlvdfskspeegksasndricieilleaerdpilgeas 411  
 QY 417 VSLAMAGESLRGRLLYLENVALARIMFPMPEARVAMDAQVDTLEFNLSGANPPPERQ 476  
 Db 412 vslamagddlrmlklylenrvglakllfpmearvamdaiaqvdgtsefplasiqkmanaq 471  
 QY 477 RFTVDLNSPFTMEHEHARMTALSKTVELGKRFPFRCSNVLDKTM--DDETFDPSVSLGRD 534  
 Db 472 rttvdineapfkikeehlnrlalrtvlgkrffprcsevlmklmdaddiseiaymgnd 531  
 QY 535 TSAE---KRRKPHDLQDVLOKAFHEDKEENDR-SGLSSSSSSSTSGAIRPRR 582  
 Db 532 taeeqrklkqymelqeilthkaftedkeydktnnisccsstsgvdkpnk 583

RESULT 6  
 AAB27324  
 ID AAB27324 standard; Protein; 604 AA.  
 AC AAB27324;  
 DT 25-JAN-2001 (first entry)  
 DE B. vulgaris NIM1 homologue SEQ ID NO: 64.  
 KW Systemic acquired resistance; SAR; signal transduction cascade;  
 KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;  
 KW potato.  
 OS Beta vulgaris.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 590  
 FT /label= Ser  
 FT /note= "encoded by TCGTCG"  
 XX  
 PN WO200053762-A2.  
 PD 14-SEP-2000.  
 PF 07-MAR-2000; 2000WO-EP01978.  
 PR 09-MAR-1999; 99US-0265149.  
 XX (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Salmeron JM, Weislo LJ, Willits MG, Mengiste T;  
 XX  
 DR WPI; 2000-594322/56.  
 DR N-PSDB; AAA97229.  
 XX  
 PT Novel plant genes for enhancing systemic acquired resistance gene  
 PT expression and broad spectrum disease resistance in plants, are  
 PT homologues of Arabidopsis NIM1 gene -  
 XX  
 PS Claim 1; Page 130-131; 152pp; English.  
 XX  
 CC The present invention is concerned with the isolation of NIM1 homologues  
 CC and their coding sequences from Arabidopsis thaliana, Brassica napus,  
 CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus  
 CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the

CC signal transduction cascade leading to systemic acquired resistance (SAR)  
 CC in plants. This gives the plants an increased resistance to disease. The  
 CC protein and gene can be used to produce transgenic plants resistant to  
 CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,  
 CC ringspot virus, petargonium leaf curl virus, red clover mottle virus,  
 CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and  
 CC peronospora tabacina, bacteria such as Pseudomonas syringae and P.  
 CC tabaci, insects, including aphids and lepidoptera and nematodes such as  
 CC Meloidogyne incognita. In particular they can be used against disease  
 CC organisms of maize.  
 XX  
 SQ Sequence 604 AA;  
 Query Match 55.2%; Score 1629; DB 21; Length 604;  
 Best Local Similarity 57.4%; Pred. No. 9.1e-145; Indels 44; Gaps 10;  
 Matches 343; Conservative 81; Mismatches 130;  
 QY 11 AFSDSDSAS-----VEEGDADADADVEALRRLSDNLAAAFR---SPED 50  
 Db 15 afsdndisngssiccvatttttttaaaenslsfpaadaallrlsenidslfqpslsld 74  
 QY 51 FAFLADARIAVPGGGGGDLRVHRCVLSARSPPFLRGVFARRAAAGGGGGDSER--- 107  
 Db 75 sdsfadakivv---sgdsrevavhrcvlsrstrsffrsafaskreke-----erdkervvk 127  
 QY 108 LELRELLGGGEEVEGYEALRLVDLYSGRVGDLPRACLCVDEDCAHVCHPAVAFM 167  
 Db 128 leikdlag-----dfevgfdsvvavigyysgkvrnlprgicvdcvdesheacrpaivd 183  
 QY 168 AQVFAASTFQVAELTNLFQRRLDLVDKVEVDNLLILSVANLCKSKMLERCLDMV 227  
 Db 184 vevlyshkfeivelvslyqrhlldikadpdlvlsvaemcgnacdgllaridki 243  
 QY 228 VRSNLDMTLEKSLPPDVIKOIIDARLSGLISPENKGFNPKHVRIHRLDSDVVELVR 287  
 Db 244 vrsldvttidklsbpqvvvkqiidtrkelgftpegrvefepdkhvkrihraldsddvelvr 303  
 QY 288 MLTETQNLDDAFALHVAHEHCDSKITTELDDALADVNHRNPRGYTVLHIAARRREP 347  
 Db 304 mlkerhttiddayalhyavahcdakttelieigladvnlrnlrghtvhlvaamrkepk 363  
 QY 348 IIVSLLTGKARPADVTFDGKAVQISKRLTKQGYFGVTEEGKSPKDRLCIEILEQAER 407  
 Db 364 iivslitkgahpsditsddkalakrltkavdyfktteggkdpakdrclcieleqaer 423  
 QY 408 RDPQLGEASVSLAMAGESLRGRLLYLENVALARIMFPMPEARVAMDAQVDTLEFNLSG 467  
 Db 424 repllgegsvs lakagddlrmlklylenvalarilfpmearvamdaiaqvdgtseftlsk 483  
 QY 468 GANPPPERQRTVVDLNSPFTMEHEHARMTALSKTVELGKRFPFRCSNVLDKIMD--DE 525  
 Db 484 ni---adarnavdineapflkeehlqmkalsktvelgkrffprcsdvlmkindeaedl 540  
 QY 526 TDPVSLGRDTSAE---KRRKPHDLQDVLOKAFHEDKEENDRSGLSSSSSSTSGAIRP 580  
 Db 541 sqlafigkdtpeergkrkryielqldaltkaftedkeefdrstlssssstpmg--rp 596

RESULT 7  
 AAG17533  
 ID AAG17533 standard; Protein; 593 AA.  
 XX  
 AC AAG17533;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 18588.  
 XX  
 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX

OS	Arabidopsis thaliana.		
XX	EP1033405-A2.	PR	30-JUN-1999;
PN		PR	01-JUL-1999;
XX		PR	01-JUL-1999;
XX		PR	02-JUL-1999;
PD	06-SEP-2000.	PR	06-JUL-1999;
XX		PR	08-JUL-1999;
PF		PR	09-JUL-1999;
XX	25-FEB-2000; 2000EP-0301439.	PR	12-JUL-1999;
XX		PR	13-JUL-1999;
PF		PR	14-JUL-1999;
PR	25-FEB-1999;	PR	15-JUL-1999;
PR	05-MAR-1999;	PR	16-JUL-1999;
PR	09-MAR-1999;	PR	16-JUL-1999;
PR	23-MAR-1999;	PR	19-JUL-1999;
PR	25-MAR-1999;	PR	19-JUL-1999;
PR	29-MAR-1999;	PR	19-JUL-1999;
PR	01-APR-1999;	PR	19-JUL-1999;
PR	06-APR-1999;	PR	19-JUL-1999;
PR	08-APR-1999;	PR	19-JUL-1999;
PR	16-APR-1999;	PR	19-JUL-1999;
PR	19-APR-1999;	PR	19-JUL-1999;
PR	21-APR-1999;	PR	20-JUL-1999;
PR	23-APR-1999;	PR	20-JUL-1999;
PR	28-APR-1999;	PR	21-JUL-1999;
PR	30-APR-1999;	PR	21-JUL-1999;
PR	04-MAY-1999;	PR	22-JUL-1999;
PR	05-MAY-1999;	PR	22-JUL-1999;
PR	06-MAY-1999;	PR	22-JUL-1999;
PR	06-MAY-1999;	PR	23-JUL-1999;
PR	07-MAY-1999;	PR	23-JUL-1999;
PR	11-MAY-1999;	PR	23-JUL-1999;
PR	14-MAY-1999;	PR	23-JUL-1999;
PR	14-MAY-1999;	PR	26-JUL-1999;
PR	14-MAY-1999;	PR	27-JUL-1999;
PR	14-MAY-1999;	PR	27-JUL-1999;
PR	18-MAY-1999;	PR	27-JUL-1999;
PR	19-MAY-1999;	PR	28-JUL-1999;
PR	20-MAY-1999;	PR	02-AUG-1999;
PR	21-MAY-1999;	PR	02-AUG-1999;
PR	24-MAY-1999;	PR	02-AUG-1999;
PR	25-MAY-1999;	PR	03-AUG-1999;
PR	27-MAY-1999;	PR	04-AUG-1999;
PR	28-MAY-1999;	PR	04-AUG-1999;
PR	01-JUN-1999;	PR	05-AUG-1999;
PR	03-JUN-1999;	PR	05-AUG-1999;
PR	04-JUN-1999;	PR	06-AUG-1999;
PR	07-JUN-1999;	PR	06-AUG-1999;
PR	08-JUN-1999;	PR	09-AUG-1999;
PR	10-JUN-1999;	PR	09-AUG-1999;
PR	10-JUN-1999;	PR	10-AUG-1999;
PR	10-JUN-1999;	PR	11-AUG-1999;
PR	14-JUN-1999;	PR	12-AUG-1999;
PR	16-JUN-1999;	PR	13-AUG-1999;
PR	16-JUN-1999;	PR	13-AUG-1999;
PR	17-JUN-1999;	PR	16-AUG-1999;
PR	18-JUN-1999;	PR	17-AUG-1999;
PR	18-JUN-1999;	PR	18-AUG-1999;
PR	18-JUN-1999;	PR	20-AUG-1999;
PR	18-JUN-1999;	PR	20-AUG-1999;
PR	18-JUN-1999;	PR	23-AUG-1999;
PR	18-JUN-1999;	PR	23-AUG-1999;
PR	18-JUN-1999;	PR	25-AUG-1999;
PR	18-JUN-1999;	PR	26-AUG-1999;
PR	18-JUN-1999;	PR	27-AUG-1999;
PR	18-JUN-1999;	PR	27-AUG-1999;
PR	21-JUN-1999;	PR	27-AUG-1999;
PR	22-JUN-1999;	PR	30-AUG-1999;
PR	23-JUN-1999;	PR	31-AUG-1999;
PR	23-JUN-1999;	PR	01-SEP-1999;
PR	24-JUN-1999;	PR	07-SEP-1999;
PR	24-JUN-1999;	PR	10-SEP-1999;
PR	29-JUN-1999;	PR	13-SEP-1999;
PR		99US-0141287.	
		99US-0141842.	
		99US-0142154.	
		99US-0142055.	
		99US-0142390.	
		99US-0142803.	
		99US-0142920.	
		99US-0142977.	
		99US-0143542.	
		99US-0143624.	
		99US-0144005.	
		99US-0144085.	
		99US-0144086.	
		99US-0144325.	
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		99US-0144352.	
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		99US-0145086.	
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		99US-0145951.	
		99US-0146386.	
		99US-0146388.	
		99US-0146389.	
		99US-0147038.	
		99US-0147204.	
		99US-0147302.	
		99US-0147192.	
		99US-0147260.	
		99US-0147303.	
		99US-0147416.	
		99US-0147493.	
		99US-0147935.	
		99US-0147935.	
		99US-0148171.	
		99US-0148319.	
		99US-0148341.	
		99US-0148565.	
		99US-0148684.	
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		99US-0149902.	
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		99US-0150566.	
		99US-0150884.	
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		99US-0151066.	
		99US-0151080.	
		99US-0151303.	
		99US-0151438.	
		99US-0151930.	
		99US-0152363.	
		99US-0153070.	
		99US-0153758.	

PR 15-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 22-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159331.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
 PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 43.5%; Score 1285; DB 21; Length 593;  
 Best Local Similarity 47.3%; Pred. No. 1.8e-115; Indels 28; Gaps 9;  
 Matches 274; Conservative 113; Mismatches 164; Indels 28; Gaps 9;

QY 5 TSHVTNAFSDSDSASVEEGDADADAEALRLSDNLAARSPEDFAFLADARIAVPGG 64  
 DB 17 tsfvtatndtssivlaaeqvtgpdvsalqlslsfsesvfdspdd--fysdaklvi--- 71  
 QY 65 GGGGDLRHVRHCVLSARSFPLRGVFAARRAAAGGCGGEGDSEERLELLGGGGEVEVG 124  
 DB 72 -sdgrvsthrvlsarsffksala--aakkekdsnmntaavkkllel---akdyevg 124  
 QY 125 YEALRLVLDVLYSGRGVLDLPKACACLVDECAHVGHCPAVAFMAQVLFASSTFOVAELTN 184  
 DB 125 fdsvtvtlayvssrvppkgvsecadcnchvacrpavdflmlevlylafripelvt 184  
 QY 185 LFQRRLLDVLKVEVDNLLILSVANLCNCKMKLERCLDMVVRNLDMLTEKSLPPD 244  
 DB 185 lqyrhldvdkviedtiulkianicgkacmkllldrcckelivksnvdmsvlskslpee 244  
 QY 245 VIKQIIDARLSGLISFENKPNKVRHRLALSDDDVVELVPMLLTEQTNLDDAFALH 304  
 DB 245 lvkeiidrrkelglevpkvk---khvsnvhkaldsddielvklldkhtnlddcalh 300  
 QY 305 YAYEHCDSTTTLLDLALADVNRHPRGTVLIHIAARREPKIIVSLTKGARPADVTF 364  
 DB 301 favaycnvktatdlldladvnhnprgrtyvlhvaaamkeqllislekgasaseatl 360  
 QY 365 DGRKAVQISKRITKOGDYGVTEEGKPSPKDRILCILEIQAERRDPOLGEASVSLAMAGE 424

DB 361 egrtalmiakqatmavecnnipqckhslkgrlcveilleqekdrepiprdvppsfavaad 420  
 QY 425 SLRGRLLYLENVALARIMFPEARVAMADIAQVDGTLEENLCSGANPPPER---QRTTV 480  
 DB 421 elkmtlldienvalaqrifpteadaamaiaemkgctcefvts---lepdlrtgkrtsp 477  
 QY 481 DLNESPIMKEEHLARMTALSKTVELGKFFPRCSNVLDKIMD-DETDPSVLSGRDTSARE 539  
 DB 478 gvkiapfrileehqsrklasktvelgkffprcsavldqimncedltqlacgeddtaek 537  
 QY 540 R---KRFHDLQVLOKAFHEKENDRSLSSSSSTS 574  
 DB 538 riqkqymeiqetlikkfatsednlelgnssldtsts 576

RESULT 8  
 AAW64435  
 ID AAW64435 standard; Protein; 593 AA.  
 XX  
 AC AAW64435;  
 XX  
 DT 16-OCT-1998 (first entry)  
 XX  
 DE A. thaliana NIM-1 protein.  
 XX  
 KW NIM-1; noninducible immunity; systemic acquired resistance; SAR;  
 KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;  
 KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide.  
 XX  
 OS Arabidopsis thaliana.  
 PN WO9829537-A2.  
 XX  
 PD 09-JUL-1998.  
 XX  
 PF 23-DEC-1997; 97WO-EP07253.  
 PR 10-JAN-1997; 97US-0035024.  
 PR 27-DEC-1996; 96US-0034378.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 XX  
 PI Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;  
 DR WPI: 1998-388119/33.  
 DR N-PSDB; AAV45273.  
 XX

Protection of immunomodulated plants against pathogens - comprises applying microbicide to provide increase in resistance  
 Claim 6; Page 103-106; 164pp; English.  
 XX  
 CC This sequence represents the NIM-1 protein from Arabidopsis thaliana.  
 CC This protein is used in a method resulting in the protection of an  
 CC immunomodulated plant having a first level of resistance and involves  
 CC treatment with at least 1 microbicide that confers a second level of  
 CC resistance, such that the plants have a third level of resistance greater  
 CC than the sum of the first two levels. The method can be applied to a wide  
 CC variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect  
 CC against viruses, fungi, bacteria, insects and nematodes. The method  
 CC provides a high level of resistance and allows a reduction in the amount  
 CC of microbicide used. Since the process involves two different methods of  
 CC protection, it is unlikely that the pathogen will develop resistance to  
 CC the treatment.

SQ Sequence 593 AA;

Query Match 43.2%; Score 1276; DB 19; Length 593;  
 Best Local Similarity 47.2%; Pred. No. 1.3e-114; Indels 28; Gaps 9;  
 Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;  
 QY 5 TSHVTNAFSDSDSASVEEGDADADAEALRLSDNLAARSPEDFAFLADARIAVPGG 64

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Db 17 tsfvtatntdssivylaaevltgpdvsalqlnsfsvfddpdd--fysdaklvi--- 71
Qy 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAGGGGDSERLELRELLGGGEEVEVG 124
Db 72 -sdgrevsfhrvlsarsffksala--aakkeksntntaavklelkei---akdyevg 124
Qy 125 YEALRLVDLYLGRVGDLPKAAACLVDECAHVCHGHPAVAFMAQVLFPAASTFOVAELTN 184
Db 125 fdsvvtvlayvysrvpppgvsecadencchvacrpavdvmlevlylafikipeit 184
Qy 185 LFQRRLLDVLKVEVDNLLILSVANLCKNSCKMLLRCERLDMVVRNSLMDITLTKSLPPD 244
Db 185 lyqrhlldvdkviedtlvilkianicgkacmklldrckeilvksnvmvslksipee 244
Qy 245 VIKQIIDARLSGLTISPENKGFPHKVRRIHRAALDSDDELVRMLLTGEGTNLDDAFALH 304
Db 245 lvkeidrrkelglevpkvk---khvsnvhkaldsddielvklkedhtnlddcaalh 300
Qy 305 YAVEHCDSKITTELLDLALADVNRHNPGRGYTVLHIAARRRPEKTIIVSLTLKGPADVTF 364
Db 301 favaycnvktatdlkldadvnrhnpgrgytvhlhvaamrkepqilslilekgsaseatl 360
Qy 365 DGRKAVQISKRLTKQGYFGVTEGKSPKDRLCIEILEQARRDPOLGEASVSLAMAGE 424
Db 361 egrtalmiakqatnavecnnpieqckshlgrlcvlelleqgedkreqipdrvpvsfavaad 420
Qy 425 SLRGRLLYLENRVALARIMFPMPEARVAMDIQAVDGTLEFNLGSGANPPPER---QRTTV 480
Db 421 elkmtdlenrvalaqrlfpteagaameiaemkgctefivts---lepdrltgkrtsp 477
Qy 481 DLNESPTFMKEEHLARMTALSKTVELGKRFPGRCSNVLDTKIMD-DETPVSLGRDTSNAEK 539
Db 478 gvkiapfrileehqsrkalsktvelgkrffprcsavidqimnceditqlacgeddtaek 537
Qy 540 R----KRFHDLQDLVLOKAFHEDKEENDRSGLSSSSSSTS 574
Db 538 rlqkqrymeiqetlkkafsednlelgnssitdatssts 576

RESULT 9
AAW46940
ID AAW46940 standard; Protein; 593 AA.
AC AAW46940;
XX
XX
XX
XX 17-AUG-1998 (first entry)
XX Arabidopsis thaliana acquired resistance protein.
KW NPRI gene; acquired resistance; disease; plant pathogens; bacteria;
KW mycoplasma; fungi; insects; nematodes; viruses; viroids;
KW transgenic.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
FT Region 252..265
FT /note= "potential nuclear localisation signal"
FT Region 541..554
FT /note= "potential nuclear localisation signal"
XX
XX WO9806748-A1.
XX
XX 19-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US13994.
XX
XX 16-MAY-1997; 97US-0046769.
PR 09-AUG-1996; 96US-0023851.
XX 10-JAN-1997; 97US-0035166;
XX
XX (GEO) GEN HOSPITAL CORP.

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PA (UYDD-) UNIV DUKE.
XX Ausubel FM, Cao H, Dong X, Glazebrook J;
XX WPI: 1998-159458/14.
DR N-PSDB; AAV16851.
XX New isolated plant acquired resistance polypeptide gene - useful
PT for, e.g. producing plants with increased resistance to pathogens
PT such as bacteria
XX Claim 26; Fig 5; 127pp; English.
XX The sequence is that encoded by the acquired resistance gene
CC NPRI. It may be produced by transgenic cells which are useful
CC in the production of plants having an increased level
CC of resistance against disease caused by plant pathogens, e.g.
CC bacteria, mycoplasmas, fungi, insects, nematodes, viruses,
CC and viroids.
XX Sequence 593 AA;
SQ
Query Match 43.2%; Score 1276; DB 19; Length 593;
Best Local Similarity 47.2%; Pred. No. 1.3e-114;
Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;
Qy 5 TSHVTNAFSDSDSASVEEGDADADADVEALRRLSDNLAAAFRSPEDFAFLADARIAPGG 64
Db 17 tsfvtatntdssivylaaevltgpdvsalqlnsfsvfddpdd--fysdaklvi--- 71
Qy 65 GGGGDLRVHRCVLSARSFPLRGVFAARRAAAGGGGDSERLELRELLGGGEEVEVG 124
Db 72 -sdgrevsfhrvlsarsffksala--aakkeksntntaavklelkei---akdyevg 124
Qy 125 YEALRLVDLYLGRVGDLPKAAACLVDECAHVCHGHPAVAFMAQVLFPAASTFOVAELTN 184
Db 125 fdsvvtvlayvysrvpppgvsecadencchvacrpavdvmlevlylafikipeit 184
Qy 185 LFQRRLLDVLKVEVDNLLILSVANLCKNSCKMLLRCERLDMVVRNSLMDITLTKSLPPD 244
Db 185 lyqrhlldvdkviedtlvilkianicgkacmklldrckeilvksnvmvslksipee 244
Qy 245 VIKQIIDARLSGLTISPENKGFPHKVRRIHRAALDSDDELVRMLLTGEGTNLDDAFALH 304
Db 245 lvkeidrrkelglevpkvk---khvsnvhkaldsddielvklkedhtnlddcaalh 300
Qy 305 YAVEHCDSKITTELLDLALADVNRHNPGRGYTVLHIAARRRPEKTIIVSLTLKGPADVTF 364
Db 301 favaycnvktatdlkldadvnrhnpgrgytvhlhvaamrkepqilslilekgsaseatl 360
Qy 365 DGRKAVQISKRLTKQGYFGVTEGKSPKDRLCIEILEQARRDPOLGEASVSLAMAGE 424
Db 361 egrtalmiakqatnavecnnpieqckshlgrlcvlelleqgedkreqipdrvpvsfavaad 420
Qy 425 SLRGRLLYLENRVALARIMFPMPEARVAMDIQAVDGTLEFNLGSGANPPPER---QRTTV 480
Db 421 elkmtdlenrvalaqrlfpteagaameiaemkgctefivts---lepdrltgkrtsp 477
Qy 481 DLNESPTFMKEEHLARMTALSKTVELGKRFPGRCSNVLDTKIMD-DETPVSLGRDTSNAEK 539
Db 478 gvkiapfrileehqsrkalsktvelgkrffprcsavidqimnceditqlacgeddtaek 537
Qy 540 R----KRFHDLQDLVLOKAFHEDKEENDRSGLSSSSSSTS 574
Db 538 rlqkqrymeiqetlkkafsednlelgnssitdatssts 576

RESULT 10
AAW23963
ID AAW23963 standard; Protein; 593 AA.
XX
XX AAW23963;
AC

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XX 17-JUN-1998 (first entry)  
 XX Arabidopsis thaliana NIM1 protein.  
 DE NIM1; noninducible immunity; disease resistance; plants;  
 KW SAR gene expression.  
 KW Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX WO9749822-A1.  
 XX 31-DEC-1997.  
 XX 10-MAR-1997; 97WO-EP01218.  
 XX 10-JAN-1997; 97US-0035022.  
 PR 21-JUN-1996; 96US-0020272.  
 PR 30-AUG-1996; 96US-0024883.  
 PR 13-DEC-1996; 96US-0033177.  
 PR 27-DEC-1996; 96US-0773559.  
 XX (NOVS ) NOVARTIS AG.  
 XX Delaney TP, Ellis DM, Friedrich LB, Johnson JE;  
 PI Lawton KA, Ryals JA, Weymann K;  
 XX WPI; 1998-077185/07.  
 DR N-PSDB; AAV04632.  
 XX NIM1 gene allows activation in plant of systemic acquired  
 PT resistance - useful to confer broad spectrum disease resistance in  
 PT plants, specifically crop plants, e.g. rice, wheat, barley, rye and  
 PT corn  
 XX Disclosure; Fig 15; 153pp; English.  
 XX The sequence is that of the NIM1 (noninducible immunity) protein. It  
 CC may be used to confer a broad spectrum disease resistance in plants,  
 CC specifically crop plants, e.g. rice, wheat, barley, rye and corn.  
 CC The NIM1 gene can be used to confer universal disease susceptibility  
 CC to plant cells, and their progeny. It can also be used in a screening  
 CC method for identifying compounds capable of inducing broad spectrum  
 CC disease resistance in plants, while the plant cells, and their  
 CC progeny, can be used to isolate a gene fragment which allows  
 CC expression of broad spectrum disease resistance in plants, or to  
 CC incorporate the resistant trait into plant lines through breeding.  
 XX SQ Sequence 593 AA;  
 Query Match 43.2%; Score 1276; DB 19; Length 593;  
 Best Local Similarity 47.2%; Pred. No. 1.3e-114;  
 Matches 273; Conservative 113; Mismatches 165; Indels 28; Gaps 9;  
 QY 5 TSHVTNFAFSDSASVEEGDADADAEALRLSDNLAARSPEDFAFLADARIAVPGG 64  
 DB 17 tsfvatndtssivylaaeqvltgpdvsalqlnsfsvfddpda--fysdakivi--- 71  
 QY 65 GGGGDLRHRCVLSARSFPLRGVFARRAAAGGGGDSERLELRELLGGGEEVEYG 124  
 DB 72 -sdgrevsfhrvcvlsarsfssklsala--aakkekdsntaavkkllelkei---akdyevg 124  
 QY 125 YEALRLVLDLYSGRVGDLPLKACLCVDEDCARHVGCHPAVAFMAQVLFPAASTFOVAELTN 184  
 DB 125 fssvvtvlayvysrvrppkvgsecadncchvacrpavdflmlevlylafikipellit 184  
 QY 185 LFQRELLDLDKVEVDNLLILSVANLCKNSCKMLERCLDMVVRNSNLDMLTLEKSLPDD 244  
 DB 185 lqrlhldvdkvvdviedtivilkianicgacmkllorcketiivsnvdmvlsleksipee 244  
 QY 245 VIKQITDARLSLGLISPENKGFNKHVRRIHRAALSDDDVELVRLMLLTEGQTNLDDAFALH 304  
 DB 245 ::::||||| ||| | : : ||| ::::|||||:|||||:||||| ||| ||| |||

DB 245 lvkeiidrrkelglevpkvk----khvsnvhkaldsddielvklilkedhtnlddcalh 300  
 QY 305 YAVEHCDSKITTELLDLALADVNNHNPGRGYTVLHIAARRREPKIIVSLTKGARPADVTF 364  
 DB 301 favaycnvxtatdlkladlvnhrnprgytvihvaamrkepqllilsllekgasaseatl 360  
 QY 365 DGRKAVOISKRLTKQGYFEGVTEEGKPSKDLCLICILBOAERRDPOLGEASVSLAMAGE 424  
 DB 361 egrtalmiakqatmavecnipeqkshkgrlcveileqekreqidrvppsfavaad 420  
 QY 425 SLRGRLLYLENRVALARIMFPMPEARVAMDIQAQVDGTLEFNLGSGANPPPER----QRTTV 480  
 DB 421 elkmtlldlenvalaqrifpteaaqaeameiaemkgctcefvts---lepdrltgkrtsp 477  
 QY 481 DLNESPFINKEEHLARMTALSKTVELGKFFPRCSNVLDKIMD-DETDVPSLGRDTSARK 539  
 DB 478 gvkiapfrileehqsrkalsktvelgkfrfcrsavlqdmncedltqlaceddtaek 537  
 QY 540 R----KRPHDLQDLVQKAFHEKDEKENDRSGLSSSSSSTS 574  
 DB 538 riqkqrymeiqetikkafsednlelgnssldststs 576  
 RESULT 11  
 AAW61982  
 ID AAW61982 standard; Protein; 593 AA.  
 XX AC. AAW61982;  
 XX DT 29-SEP-1998 (first entry)  
 DE A. thaliana non-inducible immunity-1 (NIM1) wild-type protein.  
 KW Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant;  
 KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;  
 KW constitutive immunity; agriculture.  
 XX Arabidopsis thaliana.  
 FH Key Location/Qualifiers  
 FT Misc-difference 566  
 FT /label= Ser, Ala  
 FT /note= "indicated differently in different parts of  
 the specification"  
 PN WO9826082-A1.  
 XX 18-JUN-1998.  
 XX 12-DEC-1997; 97WO-EP07012.  
 PR 20-JUN-1997; 97US-0880179.  
 PR 13-DEC-1996; 96US-0033177.  
 PR 27-DEC-1996; 96US-0034379.  
 PR 27-DEC-1996; 96US-0034382.  
 PR 10-JAN-1997; 97US-0034730.  
 PR 10-JAN-1997; 97US-0035021.  
 PR 10-JAN-1997; 97US-0035022.  
 XX (NOVS ) NOVARTIS AG.  
 XX Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HW;  
 PI Uknes SJ;  
 XX WPI; 1998-348536/30.  
 DR N-PSDB; AAV43659.  
 XX use of non-inducible immunity-1 gene - for transforming plants to  
 PT produce transgenic plants having a broad spectrum disease resistance  
 XX Example 15; Pages 108-116; 205pp; English.  
 PS This represents the Arabidopsis thaliana non-inducible immunity-1 (NIM1)  
 CC

CC wild-type protein. This can be mutated to produce altered forms of  
 CC the NIM1 protein. The invention provides a chimeric gene comprising a  
 CC promoter active in plants operatively linked to a DNA molecule that  
 CC encodes an altered form of the NIM1 protein. Plant cells stably  
 CC transformed with a recombinant vector comprising such a chimeric gene  
 CC have a broad spectrum of disease resistance. The altered NIM1 proteins  
 CC act as dominant-negative regulators of the systemic acquired resistance  
 CC (SAR) signal transduction pathway. The transgenic plants transformed with  
 CC an altered NIM1 gene exhibits constitutive SAR expression which is higher  
 CC in the transformed plants than in a wild-type plant. The products can be  
 CC used for producing plants with a broad spectrum disease resistance.  
 CC Overexpression of NIM1 mimics the effects of inducer compounds that  
 CC induce constitutive immunity (CTM) phenotype in plants. The inventions  
 CC can be used with plants such as rice, wheat, barley, rye, corn, potato,  
 CC carrot, sweet potato, sugar beet, bean, pea, chickory, lettuce, cabbage,  
 CC cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic,  
 CC eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber,  
 CC apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot,  
 CC strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya,  
 CC mango, banana, soybean, tobacco, tomato, sorghum and sugarcane. The  
 CC plants produced are resistant to plant pathogens such as viruses,  
 CC viroids, fungi, bacteria, insects such as aphids and lepidoptera and  
 CC nematodes. The plants produced can be used in agriculture.  
 XX  
 XX Sequence 593 AA;

Query Match 43.1%; Score 1272; DB 19; Length 593;  
 Best Local Similarity 47.0%; Pred. No. 3.2e-114;  
 Matches 272; Conservative 113; Mismatches 166; Indels 28; Gaps 9;

QY 5 TSHVTNAPSDDSDASVEGDADADAEALRLSDNLAAAFSPEDFAFLADARIAVPGG 64  
 DB 17 tsfvtatndtsiivylaaevltpdvlsalqlnsfsvfdspdd--fysdakivl--- 71  
 QY 65 GGGGDLRVHRCVLSARSPFLRGVFARRAAAAAGGGGDSERLELRELLGGGEEVEVG 124  
 DB 72 -sdgrevsfhrvcvlsarsffksala--aakkeksnntaavkielkei---akdyevg 124  
 QY 125 YEALRLVLDYLSGRVGLDPKALCLVDEDCAHVGCHPAVAFMAQVLPFAASTFOVAELTN 184  
 DB 125 fssvvtvlayvysrrppkvgsecadcnchvacrpavdmlevlylafikipelit 184  
 QY 185 LFORLLDLVDKVEVDNLLTSLVANLCKMCKLLERCLDMVRSNLDMLTLEKSLPPD 244  
 DB 185 lqyrhlldvdkviedtlvllkianicgkcmkldrcckeiivksndvmsleksipee 244  
 QY 245 VIKQITIDARLSGLTSPENKGPNNKHVRIHRLDSDVDVLMRLTGGQNLDDAFALH 304  
 DB 245 lvkeidrrkelglevpkvk---khvsnvhkaidssdielvklllkedhndldacalh 300  
 QY 305 YAVEHCDSKITELDLALADVNHRNPRGYTVLHTAARREPKIIVSLITKGPADVTF 364  
 DB 301 favaycnvktatdlklldadnhrnprgytvlhvaamrkepqililsilekgsaseatl 360  
 QY 365 DGRKAVQISKRLTKGDFYGVTEKPSKDRLCIEILEQAEKRPDQPGEASVSLAMAGE 424  
 DB 361 egrtalmakqatmavecnnpieqckshkgrlcvlelleqgedkreqlprdvpsfavaad 420  
 QY 425 SLRGRLLYLENVALARIMFPEARVAMDIQAVDGTLEFNILGSGGANPPPER----QRTTV 480  
 DB 421 elkmtdlidenvalaqlrfpteaaameiaemkgctcefvts---lepdrltgtkrts 477  
 QY 481 DLNESPFIMKEHLARMTALSKTVELGRFFPRCSNVLDKTMD-DETPVSLGRDTSAEK 539  
 DB 478 gvkliapfrileehqgrlkalstveigkrfprcsavldqimnoedltqlacgeedtaek 537  
 QY 540 R----KRFHDQDLVQLQAFHEDKENDRSGLSSSSSSTS 574  
 DB 538 rlqkqrymeiqetikkafsednlelgnxsltdtssts 576

RESULT 12

AAW64436  
 ID AAW64436 standard; Protein; 593 AA.  
 XX  
 AC AAW64436;  
 XX  
 DT 16-OCT-1998 (first entry)  
 XX  
 DE A. thaliana variant NIM-1 protein #1.  
 XX  
 KW NIM-1; noninducible immunity; systemic acquired resistance; SAR;  
 KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;  
 KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide.  
 XX  
 OS Arabidopsis thaliana.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 55 /label= S55A  
 FT /note= "Wild-type Ser is replaced by Ala"  
 FT Misc-difference 59 /label= S59A  
 FT /note= "Wild-type Ser is replaced by Ala"  
 FT  
 XX WO9829537-A2.  
 XX  
 XX 09-JUL-1998.  
 XX  
 XX 23-DEC-1997; 97WO-EP07253.  
 XX  
 XX 10-JAN-1997; 97US-0035024.  
 XX  
 XX 27-DEC-1996; 96US-0034378.  
 XX  
 XX (NOVS ) NOVARTIS AG.  
 XX  
 XX Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;  
 XX WPI: 1998-388119/33.  
 XX N-PSDB; AAV46275.  
 XX  
 XX Protection of immunomodulated plants against pathogens - comprises  
 XX applying microbicide to provide increase in resistance  
 XX  
 XX Claim 10; Page 120-123; 164pp; English.  
 XX  
 XX This sequence represents a variant NIM-1 protein from Arabidopsis  
 XX thaliana. This protein is used in a method resulting in the protection of  
 XX an immunomodulated plant having a first level of resistance and involves  
 XX treatment with at least 1 microbicide that confers a second level of  
 XX resistance, such that the plants have a third level of resistance greater  
 XX than the sum of the first two levels. The method can be applied to a wide  
 XX variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect  
 XX against viruses, fungi, bacteria, insects and nematodes. The method  
 XX provides a high level of resistance and allows a reduction in the amount  
 XX of microbicide used. Since the process involves two different methods of  
 XX protection, it is unlikely that the pathogen will develop resistance to  
 XX the treatment.  
 XX  
 XX Sequence 593 AA;  
 SQ

Query Match 43.0%; Score 1270; DB 19; Length 593;  
 Best Local Similarity 47.0%; Pred. No. 5e-114;  
 Matches 272; Conservative 113; Mismatches 166; Indels 28; Gaps 9;

QY 5 TSHVTNAPSDDSDASVEGDADADAEALRLSDNLAAAFSPEDFAFLADARIAVPGG 64  
 DB 17 tsfvtatndtsiivylaaevltpdvlsalqlnsfsvfdspdd--fysdakivl--- 71  
 QY 65 GGGGDLRVHRCVLSARSPFLRGVFARRAAAAAGGGGDSERLELRELLGGGEEVEVG 124  
 DB 72 -sdgrevsfhrvcvlsarsffksala--aakkeksnntaavkielkei---akdyevg 124



QY 425 SLRGLLYENRVALARIMFPEARVAMIAQVDGTLFNLGSGANPPPER---QRTTV 480  
 Db 421 elktlidlennvalaqlrftaqaameiaemktcefiivs--lepdrllgtkrtsp 477  
 QY 481 DLNESPIMKEEHARMTALSKTVELKRPFGCSNVLDKIMD-DETDVPSLGRDTSK 539  
 Db 478 gvkiaptriieehqsrkalsktvelgrfprcsavldgmnceditqlacgedtdaek 537  
 QY 540 R---KEFHLDLVLOKAFHEKENDRSGLSSSSSSSTS 574  
 Db 538 rlqkqymelqetikkafsednlgnlsitdststs 576

RESULT 14  
 AAB27303 standard; Protein: 579 AA.

AC AAB27303;

DT 25-JAN-2001 (first entry)

XX B. napus NIM1 homologue SEQ ID NO: 6.

DE Systemic acquired resistance; SAR; signal transduction cascade;  
 KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;  
 KW potato.

OS Brassica napus.

XX WO200053762-A2.

XX 14-SEP-2000.

XX 07-MAR-2000; 2000WO-EP01978.

XX 09-MAR-1999; 99US-0265149.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;

XX WPI; 2000-594322/56.

XX N-PSDB; AAA97192.

PT Novel plant genes for enhancing systemic acquired resistance gene  
 PT expression and broad spectrum disease resistance in plants, are  
 PT homologues of Arabidopsis NIM1 gene -

XX Claim 1; Page 80-81; 152pp; English.

XX The present invention is concerned with the isolation of NIM1 homologues  
 CC and their coding sequences from Arabidopsis thaliana, Brassica napus,  
 CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus  
 CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the  
 CC signal transduction cascade leading to systemic acquired resistance (SAR)  
 CC in plants. This gives the plants an increased resistance to disease. The  
 CC protein and gene can be used to produce transgenic plants resistant to  
 CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,  
 CC ringspot virus, perlongonum leaf curl virus, red clover mottle virus,  
 CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and  
 CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.  
 CC tabaci, insects, including aphids and lepidoptera and nematodes such as  
 CC Meloidogyne incognita. In particular they can be used against disease  
 CC organisms of maize.

XX Sequence 579 AA;

Query Match 41.4%; Score 1222.5; DB 21; Length 579;  
 Best Local Similarity 45.9%; Pred. No. 1.9e-109;  
 Matches 260; Conservative 110; Mismatches 160; Indels 37; Gaps 10;

QY 14 DSDSASVEEGDADADADVEALRRLSDNLAAAFSPEDFAFLADARIAVPGGGGGDLRV 73  
 Db 27 nsgstvxptelxtrpvsafqlslslesvfdspe--afysdaklavl----sddkevsf 80  
 QY 74 HRCVLSARSFPLRGVTFARRAAAGGGGEGCSERLERELLGGGGEVEGYEALRLVLD 133  
 Db 81 hrcillsars-----lffkaalxaaekvqskpvtklektl----aaeydvfgdsvavla 131  
 QY 134 YLSGSRVGLPKAACLCVDECAHVGCHPAVAFMAOVLFFAASTFOVAELNLRQLLDV 193  
 Db 132 yvysgrvrpppkvscadxcchvacrpavdmvevlylafvfqqlvmqgrhllvd 191  
 QY 194 LDKVEVDNLLILSVANLCKNCKMLERCLDMVVRNLDMLTLEKSLPPDVIKIIDAR 253  
 Db 192 vdkvxiiedtlvklanicgackkifdcreiivksnvdvtklslpexiakqvidir 251  
 QY 254 LSLGLISPENKGFPHVRIHRLSDSDVELVRLMLTEGOTNLDLDAFALHYAVEHCDSK 313  
 Db 252 kelglevae---pekhsvsnihkalesddldlvmllikeghtnldeayalhfvaycdek 307  
 QY 314 ITTELDDALADVNHNRPRGTYVLHIAARRRPEKIIIVSLTKGARPADVTFDGRKAVQIS 373  
 Db 308 tarllieglfadvnrrnprgrtyvihuamrkeptliallltkganalemsldgrtallia 367  
 QY 374 KRUTKQDYEGVTEEGKPSKRLCICILQABER-RDPQLGEASVSLAMAGESLGRLLY 432  
 Db 368 kvtkaaecc-ilekgklaakgvceilkpndntrepfedvpslvaadqfkrilid 426  
 QY 433 LENRVALARIMFMEARVAMDIQVDGTLFNLGSGANPPPERQRTTVDLNESPFIMKEE 492  
 Db 427 lenrvqmarclypmeaqvamdfarmkgtrfsv-----ttatdlhmeprfkfvm 475  
 QY 493 HLAARMTALSKTVELKRPFGCSNVLDKIMDDE--TDPVSLGRDT---SAEKRRRPHDLQ 547  
 Db 476 hqsriltalsktvfgkrffprcskvladiivdsedltlaiveedtpqgrqgrfmeiq 535  
 QY 548 DVLOKAFHEKENDRSGLSSSSSSSTS 574  
 Db 536 eivgmfskdkedlgkslsassts 562

RESULT 15

AAB27307 standard; Protein: 600 AA.

AC AAB27307;

XX 25-JAN-2001 (first entry)

XX A. thaliana NIM1 homologue SEQ ID NO: 20.

XX Systemic acquired resistance; SAR; signal transduction cascade;  
 KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;  
 KW potato.

XX Arabidopsis thaliana.

XX WO200053762-A2.

XX 14-SEP-2000.

XX 07-MAR-2000; 2000WO-EP01978.

XX 09-MAR-1999; 99US-0265149.

XX (NOVS ) NOVARTIS AG.

XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Salmeron JM, Weislo LJ, Willits MG, Mengiste T;

XX WPI; 2000-594322/56.

XX N-PSDB; AAA97202.

Search completed: July 12, 2001, 17:13:31  
Job time: 53 sec

PT Novel plant genes for enhancing systemic acquired resistance gene  
PT expression and broad spectrum disease resistance in plants, are  
PT homologues of Arabidopsis NIM1 gene -

PS Claim 1; Page 98-100; 152pp; English.

The present invention is concerned with the isolation of NIM1 homologues and their coding sequences from *Arabidopsis thaliana*, *Brassica napus*, *Nicotiana tabacum*, *Lycopersicon esculentum*, *Beta vulgaris*, *Helianthus annuus* and *Solanum tuberosum*. NIM1 is one of the proteins involved in the signal transduction cascade leading to systemic acquired resistance (SAR) in plants. This gives the plants an increased resistance to disease. The protein and gene can be used to produce transgenic plants resistant to diseases caused by viruses, such as tobacco or cucumber mosaic virus, ringspot virus, perargonium leaf curl virus, red clover mottle virus, tomato bushy stunt virus, fungi, including *Phytophthora parasitica* and *Peronospora tabacina*, bacteria such as *Pseudomonas syringae* and *P. tabaci*, insects, including aphids and lepidoptera and nematodes such as *Meloidogyne incognita*. In particular they can be used against disease organisms of maize.

AA  
SQ  
Sequence 600 AA;

Query Match	41.1%	Score 1213.5;	DB 21;	Length 600;
Best Local Similarity	45.8%;	Pred. No. 1.5e-108;		
Matches 277;	Conservative 105;	Mismatches 172;	Indels 51;	Gaps 17;
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QY	47	SPEDFAFIADARIAPVGGGGGDLRVHRCVLSARSPFLRGVFARRAAAAAGGGEGDSE 106		
Db	61	spe--tfysdaklvy---aggrevsfrcilsarip----vf-ksalatvkeqksttv 109		
QY	107	RLREULLGGGGEVEVGYEARLVRDLYLSGRVGDLPKAAACLVDEDCAHVGGCHPAVAF 166		
Db	110	klqlkei-----ardveyfdsvavlayvygsvrpsppkgasacvddccchvacrskvdf 165		
QY	167	MAQVLFRAASTFOVAELNLFORRLLDVLDKVEVDNLLILLILSVANLCNSCKMLLERCLDM 226		
Db	166	mvevlylsfvqlgelvtlyerqflevkvvvedilvifkldtlcgttykklldrciel 225		
QY	227	VVRGNLDWITLTKSLPPDVIKOIIDARLSGLISPENKGFNKHVRRTHRALDSDDDVELV 286		
Db	226	ivksdievlsleklspphifqiidiid <del>l</del> lecpkpie-----rivnklykaldsddvelv 281		
QY	287	RMLTETGQTNLDADFALHYAVEHCDSKITTELLDLALADVNRHPRGYTVLHIAARREP 346		
Db	282	kmllileghtnldeayalhfaiahcavktaydlleleladvnlrnpgrtyvlhvvaamrkep 341		
QY	347	KIIVSLTLTKGARPADVTDFDGKAKVOISKRLLTKQGDYFGVTVEEGSPKDRLCIELEQAE 406		
Db	342	klilislmkganiliddtlldgrtalvivkrltkaddyktstedgtpslkggicievleh-e 400		
QY	407	RDRDQLG--EASVSIAMAGESLRGLLYLENRVALARIMPMEARVAMDIAQVDTGLEFN 464		
Db	401	qkleylspieaslsipvtpeelrmlryenvalarllfpvetqvqgiakleetceft 460		
QY	465	LGSGANPPPE--RQRTVVDLNSPFIKKEEHLARMTALSKTVELGKRFPPRCSNVLDKIM 522		
Db	461	-asslepddhlgkrtaldlmmafqihkehlsrlralcktvclgkyrfkrccs--ldhfm 517		
QY	523	DDE--TDPVSLGRDT----SAEKRRKRFDLDQVLQAFHDEKENDRSLGSSSSSTIGA 577		
Db	518	dtedlnhlasveedtpkrlqkkrymelqetlmtktfseedkee--cgkssstppts--a 572		
QY	578	IRPRR 582		
Db	573	vsrnr 577		

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2001, 07:14:42 ; Search time 1544.62 Seconds  
(without alignments)  
12484.508 Million cell updates/sec

Title: US-09-294-539-3  
Perfect score: 2040  
Sequence: 1 atggagccgaccagcca.....caaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

## EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
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6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



RESULT	1				
BG464249					
LOCUS		614 bp	mrna	EST	20-MAR-2001
DEFINITION		EM1_71.D12.b1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA sequence.			
ACCESSION		BG464249			
VERSION		BG464249.1	GI:13392562		
KEYWORDS		EST.			
SOURCE		sorghum.			
ORGANISM		Sorghum bicolor			
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.			
REFERENCE		1 (bases 1 to 614)			
AUTHORS		Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.			
TITLE		An EST database from Sorghum: developing embryos			
JOURNAL		Unpublished (2000)			

```

Db 608 GCTTAG 614

RESULT 2
LOCUS BE493178 455 bp mRNA EST 16-APR-2001
DEFINITION WHE0570_C11_F22E Triticum monococcum vegetative apex cDNA library
Triticum monococcum cDNA clone WHE0570_C11_F22, mRNA sequence.
ACCESSION BE493178
VERSION WHE0570_C11_F22
KEYWORDS Triticum monococcum
SOURCE Triticum monococcum
ORGANISM Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticaceae; Triticum.
REFERENCE 1 (bases 1 to 455)
AUTHORS Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S., Hsia
,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L.,
Stamove,B. and Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Vegetative apex cDNA library from Triticum monococcum
Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510595773
Fax: 5105959818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene T3 primer.
FEATURES
source
Location/Qualifiers
1..455
/organism="Triticum monococcum"
/cultivar="DW92"
/db_xref="taxon:4568"
/clone="WHE0570_C11_F22"
/clone_lib="Triticum monococcum vegetative apex cDNA
library"
/tissue_type="Vegetative shoot apex"
/dev_stage="Three weeks-old plants"
/lab_host="E. coli XL0L"
/note="Vector: Lambda pBK-CMV (Lambda Zap Express),
excised phagemid; Site 1: EcoRI; Site 2: XhoI; The tissue,
total RNA, and poly(A) RNA were prepared, a cDNA library
was made, and the cDNA clones were in vivo excised at the
University of California, Davis (V. Echenique, B. Stamova
, J. Dubcovsky). Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
BASE COUNT 132 a 94 c 98 g 131 t
ORIGIN
Query Match 17.3%; Score 352.6; DB 136; Length 455;
Best Local Similarity 85.9%; Pred. No. 7.6e-74;
Matches 391; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 602 acctctattgattctatctgttgcacattatgcaacaaatcttgcgatgaactgttg 661
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 1 ACCTTCGGTGTGATCTATCTGTGTGCAACTTATGCAACAAATCTTGCGTGAACACTGTTG 60

Qy 662 aaagatgccttgatagtagtccggtcaaaccttgacattactcttgagaagtcac 721
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 61 AGAGATGCGCTGGAGATGGTAGTCCGGTCAATCTTGACATGATTAATCTTGAGAAAGCAT 120

Qy 722 tgcctccagatgttatcaagcagagattattgatgcgcgcctcagccctcgattattccac 781
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 121 TGCCTGAAGATGTTATCAAGCAAAATTATTGATTCAGGATAACTCTTGATTAAGTTCAC 180

Qy 782 cagaaaaaaggagggttctcttaacaacatgtgaggaggatatacacagagcccttgactctg 841

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Db 181 CCGAAGACAATGGCTGTCTCTCAACAAACACGCTAAGAAGGACTCAAGGCACCTGATTCTG 240
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Qy 842 acgatgtagagctagtagcagatgctctgaactgaaggaagacaaatcttgatgatgcgt 901
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 241 ATGATGTGGAGCTTGTGAGGATGCTGCTACAGAAGGGCAGACTAACCTTGATGATGCAT 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Qy 902 ttgactgcactacgcgctgcaacattgtgactccaaaattcaaacgcgacttttgatc 961
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Db 301 TTGCATTGCACATATGCTGTAGAACACTGTGACACACCTGACACAAATTAACAGAACTTCTG 360
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Qy 962 tcgcacttcagatgttataatcatagaaacccaaagaggttatactgttcttcacattgctg 1021
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Db 361 TCGCATTGCGGATGTTAATCTCAGAAACCCAAAGAGGTTATACTGTCTTCCATCGCTG 420
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Qy 1022 cgaggcgaagagagcgtataaatcatgtctccctt 1056
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Db 421 CTAGGGGGAGAGATCCCTAAATAATTGTTGCTCTTCCTT 455
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RESULT 3
LOCUS BG464574 666 bp mRNA EST 20-MAR-2001
DEFINITION EMI_71_D12_g1_A002 Embryo 1 (EM1) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION BG464574
VERSION BG464574.1 GI:13393216
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 666)
AUTHORS Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
An EST database from Sorghum: developing embryos
Unpublished (2000)
TITLE Department of Botany
JOURNAL The University of Georgia
COMMENT Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: PolyTMix
High quality sequence start: 32
High quality sequence stop: 664
POLYA-No.
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Location/Qualifiers
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/db_xref="taxon:4558"
/clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2:
EcoRI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
BASE COUNT 163 a 160 c 176 g 167 t
ORIGIN
Query Match 10.5%; Score 213.6; DB 154; Length 666;
Best Local Similarity 79.8%; Pred. No. 1.5e-40;
Matches 265; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

Qy 1392 cctgggttctgtgtaaacatccacacctctgaaagacacgacgaactgttgatctaaatga 1451
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Db 2 CCTTGGTTCTTAATGCTAATCTGCCTACCGAGATTCAGCGGACA---GTTGACCTGAACGA 58

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Db	169	TGCTTTTGAAAGAGGATCACACAATCTAGATGATGCGGTGCTCTTCATTCCTCCTGTTG	228
QY	923	aacatttgactccaaaattacaaccgagctttggatctgcgaccttcgagatgttaac	982
Db	229	CATATTGCAATGTGAAGACC CGCAACAGATCTTTTTAAAACTTTGATCTTCCGCGATGCAACC	288
QY	983	atagaiaaacccagagggttactgttcttcacattgctgcgagcgcaagagagccta	1042
Db	289	ATAGGAATCCGAGGGGATATACGGTGCTCATGTGTGCTGCGATCGGAAGGAGGCCAACAT	348
QY	1043	tcattgtccccttttaaccaagggggtcgcaccagcagatgttacattcgatgggaga	1102
Db	349	TGATATCTATCTCTATTGGAAAAGGTGCAAGTGCATCAGAAGCAACTTTGGAAGTGAGAA	408
QY	1103	aagcggttcaaattcctcaaaagactacaacaaagggttactttgggtttaccgaag	1162
Db	409	CCGCACCTCATGTCGCAAAACAAAGCCACTATGCGCGTTGAATGTAATAATATCCCGAGC	468
QY	1163	aaggaiaaaccttctccaaagagttaggttatgtattgaataactcggagcaagctgaagaa	1222
Db	469	AATCGAAGCATTTCTCTCAAAGCCGCACTATGTGTAGAATACTTAGCAAGAAGACAAAC	528
QY	1223	ggagcccaactcggagaagcatcagtttcttcttcgaatggcag	1267
Db	529	GAGAACAATTTCTAGAGATGTTCTCCCTCTTTTTCAGTGGCGG	573
RESULT	5	.	
AW160235/c			
LOCUS			
DEFINITION			
AW160235	613 bp	mRNA	EST 08-NOV-1999
EST290093 L. pennellii trichome, Cornell University Lycopersicon			
pennellii cDNA clone cLPT119 similar to A. thaliana transcription			
factor inhibitor I kappa B homolog, mRNA sequence.			
AW160235			
AW160235.1	GI:6279769		
EST.			
Lycopersicon pennellii.			
Lycopersicon pennellii			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;			
Lycopersicon.			
1 (bases 1 to 613)			
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.,			
Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fuj			
,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Marti			
,G.B., Tanksley,S.D. and Giovannoni,J.			
Generation of ESTs from wild tomato (Lycopersicon pennellii)			
trichomes			
Unpublished (1999)			
Contact: David Frisch			
Clemson University Genomics Institute			
Clemson University			
100 Jordan Hall, Clemson, SC 29634, USA			
Tel: 864 656 4366			
Fax: 864 656 4293			
Email: dfrisch@CLEMSON.EDU			
3 prime sequence.			
FEATURES			
source			
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/clone="cLPT119"			
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/dev_stage="mixed stages"			
/lab_host="SOLR"			
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:			







ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

sorghum.  
Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC





QY 1157 ccgaagaagaaacacctctccaaagataggttatgtattgaataactggag 1209  
 Db 427 TGGACGAGGTCAAGATCAATAAAGATAGGCTGTGTATAGATATTCTAGAG 479

RESULT 14  
 AW310982/c  
 LOCUS  
 DEFINITION sg31b02.x1 Gm-cl024 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-cl024-2212 3' similar to TR:081848 081848 HYPOTHETICAL 68.2 KD  
 PROTEIN. ; mRNA sequence.

ACCESSION AW310982  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM soybean.  
 Glycine max

REFERENCE 1 (bases 1 to 645)  
 AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Corvelli,V., Khanna  
 ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
 ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
 ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
 ,R., Waterston,R. and Willson,R.  
 Public Soybean EST Project  
 Unpublished (1999)  
 CONTACT: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

COMMENT This clone is available through: Genome Systems, Inc. 4633 World  
 Parkway Circle St. Louis, Missouri 63134 For further information  
 call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)  
 427-3324 or contact: clones@genomesystems.com or  
 info@genomesystems.com web site: www.genomesystems.com  
 High quality sequence stop: 477.

FEATURES  
 Location/Qualifiers  
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 /lab\_host="DH10B"  
 /note="Vector: pT7T3Pac (pT7T3, Pharmacia); Site\_1: EcoRI;  
 Site\_2: XhoI; This cDNA library was constructed from mRNA  
 isolated from etiolated hypocotyl tissue of 9-10 day old  
 seedlings. Complementary DNA was synthesized from mRNA  
 using a poly (dT) primer with a XhoI restriction site.  
 EcoRI adapters were ligated to the blunt-ended cDNA  
 fragments followed by digestion with EcoRI and XhoI. The  
 cDNA fragments were directionally cloned into the  
 EcoRI-XhoI restriction site of the pT7T3-Pac vector. The  
 ligated cDNA fragments were transformed into DH10B host  
 cells (Gibco BRL). This library was constructed by Dr.  
 Randy Shoemaker."

BASE COUNT 174 a 146 c 128 g 197 t  
 ORIGIN

Query Match 6.5%; Score 133.2; DB 114; Length 645;  
 Best Local Similarity 57.6%; Pred. No. 2.6e-21;  
 Matches 303; Conservative 0; Mismatches 208; Indels 15; Gaps 3;

QY 1219 agaaggaccacactcgaagaagcatcagttctcttcgcaatggcaggtgagatcta 1278  
 Db 633 AGGAGGAATCCAATGGCTGGGATGGCTGTATGCTTCTCCATACCATGGCTGATGATCTC 574

QY 1279 cgagaaggttgctgtatcttgaacaccaggttgctttggcgaagattatgtttccgatg 1338  
 Db 573 ACATGCAAACTACTGTACCTTTGAGAACAGAGTGGCAATTTTGCAGACACTTTTCTTCCCTTCA 514

QY 1339 gaggcaagagtagcaatggatattgctcaagtggatggaaacttttgaatttaaacctgggt 1398  
 Db 513 GAAGCCAAACTAGCCATGGACATTTGGCATGCTGTGACACAACATCTCAGTTTGGTGTCTT 454

QY 1399 tctgtgtcaaatcc---acctctgaagaacacagcaactgttgcattataaataaagt 1455  
 Db 453 TCTGCGTCAAACTCAAAAGGTTCAAAATGGAATTTAAAGGAGGTTGATCTCAATGAGACT 394

QY 1456 cttttcataatgaagaagaacacttagctcggtatgacagcactctccaaaacagtgag 1515  
 Db 393 CCTATAGTCAAAATAAAGACTTCTTTAGTAATGGAAGCCCTTACGAAAACAGTGGAG 334

QY 1516 ctgggaaacgctttttcccgatgttccgaacgtgctcgacaagatcatggatgatga- 1574  
 Db 333 ATGGGCGCGCTACTTCCACATTTCTCGGAAGTCTCGACAAGTTTCATGGAGGATGAC 274

QY 1575 --aactgataccggtttccctcggaagacagctccgcggagaag-----aggaag 1623  
 Db 273 CTGCGTGAAGTGTGTTTACCTTGAAGAGGGTACTCATGAAGAGCAGAGAAATCAAAAGGACG 214

QY 1624 aggtttcatgactgcagatgttcttcgaagcattccacagagcagaaggaggagaat 1683  
 Db 213 CGTTTCATGGAGCTTAAAGATGACGTCCCAAGGCTTTCAACAAAGGACAAAGCCGAGTTT 154

QY 1684 gcaggtcggggtctctcgctcgctcgatgcacatcgatcgagg 1729  
 Db 153 AGCCGCTCTGGGATTTTCATCTTCATCATCTCATCTCATCTCAGAG 108

RESULT 15  
 AI442277  
 LOCUS  
 DEFINITION sa66a04.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-cl004-4231 5' similar to TR:P93002 P93002 REGULATORY PROTEIN  
 NPRI. ; mRNA sequence.

ACCESSION AI442277  
 VERSION  
 KEYWORDS  
 SOURCE soybean.  
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 430)  
 AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Corvelli,V., Khanna  
 ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
 Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
 ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
 ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
 ,R., Waterston,R. and Willson,R.  
 Public Soybean EST Project  
 Unpublished (1999)  
 CONTACT: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

COMMENT This clone is available through: Genome Systems, Inc. 4633 World  
 Parkway Circle St. Louis, Missouri 63134 For further information  
 call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)  
 427-3324 or contact: clones@genomesystems.com or  
 info@genomesystems.com web site: www.genomesystems.com  
 Insert Length: 1276 Std Error: 0.00  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 406  
 POLYA-No.



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2001, 07:16:22 ; Search time 2704.67 Seconds  
(without alignments)  
11666.565 Million cell updates/sec

Title: US-09-294-539-3  
Perfect score: 2040  
Sequence: 1 atgagccgacgacgcca.....caaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues  
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_ba2:  
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4: gb\_in1:  
5: gb\_in2:  
6: gb\_in3:  
7: gb\_om:  
8: gb\_ov:  
9: gb\_pat1:  
10: gb\_pat2:  
11: gb\_ph:  
12: gb\_pl1:  
13: gb\_pl2:  
14: gb\_pl3:  
15: gb\_pl4:  
16: em\_ba1:  
17: em\_ba2:  
18: em\_fun:  
19: em\_htgo\_hum:  
20: em\_htgo\_inv:  
21: em\_htgo\_rod:  
22: em\_htg\_hum1:  
23: em\_htg\_hum2:  
24: em\_htg\_hum3:  
25: em\_htg\_hum4:  
26: em\_htg\_hum5:  
27: em\_htg\_hum6:  
28: em\_htg\_hum7:  
29: em\_htg\_hum8:  
30: em\_htg\_inv1:  
31: em\_htg\_inv2:  
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33: em\_htg\_rod:  
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36: em\_hum3:  
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39: em\_hum6:  
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89: gb\_pr5:  
90: gb\_pr6:  
91: gb\_pr7:  
92: gb\_pr8:  
93: gb\_pr9:  
94: gb\_r01:  
95: gb\_r02:  
96: gb\_in4:  
97: gb\_pr10:  
98: em\_ba3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
C 1	750	36.8	140304	13	AP002537 Oryza sat
C 2	750	36.8	168372	13	AP002746 Oryza sat
C 3	422.2	20.7	2104	14	ATU76707 Arabidopsis
4	420.6	20.6	2011	9	AR087502 Sequence
5	420.6	20.6	2011	9	AR087503 Sequence
6	411.8	20.2	1608	9	AR087505 Sequence
7	409.2	20.1	1597	9	AR087504 Sequence
8	400.4	19.6	1194	9	AR087506 Sequence



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KAEALPSIWLWISOETSAHAGSLKRLKNAWLSVDGLKIMPNTLHTLEPIR
LDEDLKNLNEFCQIILNLGVGLKDPKHLHQKTCRWGSEVNVPSRLTIRAPNL
VRLKLCVPMILIDTPSMFTLKLTVKDPNVQADGLVSLKRLIESLIDLSLIQV
FAENHDITLLELESTNNKYLEFAVKPEYLQLOFAGISEVKLAPRFSCENTHCLML
CTSNQPSRCLRLHPLPLKDVPHLAPLNNCAPSCEVTILFHADSSDDIRQAATSV
WILRPGIRWQWGN"
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15388..15503,15664..15819,16008..16116,16591..16700,
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complement(join(14597..14704,14802..14932,15057..15223,
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LLVNFCKPDRKWESEDAIILKPIVPCDEIFRYRNKMEFSFGTKRWOREKEEKDD
EVYKEKVGSDYSLGHAPGDFDKVHLVEKLLQSEPADKVLAIQVETWLPALGLT
PIDVHKVGLHLMIRGNITGAPEVNVFVNSCYRPELLEPLVNNITKIPEVVS
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GESAGLKGSDIILDCFTGTLGLARRAKHYGYEVVPEAIAADKKNALKNIS
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LGRGPHVAPLPQVTVRRYLFRRPPA"
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TITLE The Arabidopsis NPR1 gene that controls systemic acquired resistance encodes a novel protein containing ankyrin repeats
JOURNAL Cell 88 (1), 57-63 (1997)
MEDLINE 97148688
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TITLE Direct Submission

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 JOURNAL Monsanto Co. (US)  
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ACCESSION	AX049431
VERSION	AX049431.1
KEYWORDS	bread wheat. Triticum aestivum
SOURCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Triticum.
REFERENCE	1 (bases 1 to 1830)
AUTHORS	Bouqri,O.V., Rommens,C.M., Srivastava,N. and Swords,K.M.

[illegible]





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AX049430

LOCUS

DEFINITION

AX049430

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1824 bp

Sequence 5 from Patent WO0070069.

GI:12226157

bread wheat.

Triticum aestivum

Eukaryote; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Triticeae; Triticum.

1 (bases 1 to 1824)

Bougril,O.V., Rommens,C.M., Srivastava,N. and Swords,K.M.

Acquired resistance genes in plants

Patent: WO 0070069-A 5 23-NOV-2000;

Monsanto Co. (US)

Location/Qualifiers

1. .1824

/organism="Triticum aestivum"

/db\_xref="taxon:4565"

FEATURES

source

438 a 478 c 512 g 396 t



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Db 1801 TTCCCAAACTGCTCGCAGGTGCTCGACAAATTC TTGGAAGATG 1843

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Job time: 8791 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2001, 07:21:13 ; Search time 102.79 seconds  
(without alignments)  
3676.730 Million cell updates/sec

Title: US-09-294-539-3  
Perfect score: 2040  
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Gapop 10.0 , Gapext 1.0

Searched: 317530 seqs, 92630169 residues

Total number of hits satisfying chosen parameters: 635060

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	411.8	20.2	1608	2	US-08-989-478-11
6	411.8	20.2	1608	3	US-08-996-685-11
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20	81	4.0	12001	1	US-08-458-568A-11
21	79.2	3.9	1931	2	US-09-130-114-2
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25	74.4	3.6	459	2	US-08-387-942C-9
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38	68.2	3.3	1845	4	US-09-029-603-5	Sequence 5, Appl
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44	67.8	3.3	1485	2	US-08-479-041-23	Sequence 23, Appl
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ALIGNMENTS

RESULT 1  
US-08-989-478-6  
; Sequence 6, Application US/08989478  
; Patent No. 5986082  
; GENERAL INFORMATION:  
; APPLICANT: Uknes, Scott  
; APPLICANT: Hunt, Michelle  
; APPLICANT: Steiner, Henry-York  
; APPLICANT: Ryals, John  
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING  
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: No. 5986082artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: No. 5986082th Carolina  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,478  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/033,177  
; FILING DATE: 13-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,379  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,382  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,730  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,021  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,022  
; FILING DATE: 10-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: PF/5-21214/PI/CGC1911



RESULT 2  
 US-08-989-478-7  
 ; Sequence 7, Application US/08989478  
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 ; GENERAL INFORMATION:  
 ; APPLICANT: Uknes, Scott  
 ; APPLICANT: Hunt, Michelle  
 ; APPLICANT: Steiner, Henry-York  
 ; APPLICANT: Ryals, John  
 ; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING  
 ; DISEASE RESISTANCE IN PLANTS  
 ; NUMBER OF SEQUENCES: 32  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: No. 5986082artis Corporation  
 ; STREET: 3054 Cornwallis Road  
 ; CITY: Research Triangle Park  
 ; STATE: No. 5986082th Carolina  
 ; COUNTRY: USA  
 ; ZIP: 27709  
 ; COMPUTER READABLE FORM:  
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 ; FILING DATE: 10-JAN-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/035,022  
 ; FILING DATE: 10-JAN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meigs, J. Timothy  
 ; REGISTRATION NUMBER: 38,241  
 ; REFERENCE/DOCKET NUMBER: PF/5-21214/PI/CGC1911  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (919) 541-8587  
 ; TELEFAX: (919) 541-8689  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2011 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
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 ; OTHER INFORMATION: /note= "Serine residues at amino acid positions 55 and 59 in  
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 ; FEATURE:  
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 ; OTHER INFORMATION: /note= "nucleotides 205 and 217

; OTHER INFORMATION: changed from T's to G's compared to wild-type sequence."  
 US-08-989-478-7

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RESULT 3

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US-08-996-685-6
; Sequence 6, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Rues, Wilhelm
; APPLICANT: Knauf-Beiter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:

```

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; ADDRESSEE: No. 6031153artis Corporation
; STREET: 3054 Cornwellis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543
; FILING DATE: 6-DEC-1996
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; FILING DATE: 27-DEC-1996
; APPLICATION NUMBER: US 60/034,379
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..2011
; OTHER INFORMATION: /note= "NIM1 cdna sequence"
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; NAME/KEY: CDS
; LOCATION: 43..1824
; OTHER INFORMATION: /product= "NIM1 protein"
; US-08-996-685-6

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Best Local Similarity 56.0%; Pred. No. 2.2e-82;
Matches 979; Conservative 0; Mismatches 704; Indels 66; Gaps 7;

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RESULT 6  
US-08-996-685-11  
: Sequence 11, Application US/08996685  
: Patent No. 6031153  
: GENERAL INFORMATION:  
: APPLICANT: Ryals, John  
: APPLICANT: Friedrich, Leslie  
: APPLICANT: Uknes, Scott  
: APPLICANT: Molina, Antonio  
: APPLICANT: Ruess, Wilhelm  
: APPLICANT: Knauf-Beiter, Gertrude  
: APPLICANT: Kung, Ruth  
: APPLICANT: Kessmann, Helmut  
: APPLICANT: Oostendorp, Michael  
: TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
: NUMBER OF SEQUENCES: 32  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: No. 6031153artis Corporation  
: STREET: 3054 Cornwallis Road  
: CITY: Research Triangle Park  
: STATE: No. 6031153th Carolina  
: COUNTRY: USA  
: ZIP: 27709  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/996,685  
: FILING DATE:  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/761,543  
: FILING DATE: 6-DEC-1996  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 60/034,378  
: FILING DATE: 27-DEC-1996  
: PRIOR APPLICATION DATA:  
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: FILING DATE: 27-DEC-1996  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 60/034,382  
: FILING DATE: 27-DEC-1996  
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: FILING DATE: 10-JAN-1997  
: PRIOR APPLICATION DATA:  
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: FILING DATE: 10-JAN-1997  
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: FILING DATE: 10-JAN-1997  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 60/035,024  
: FILING DATE: 10-JAN-1997  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/875,015  
: FILING DATE: 16-JUL-1997  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Meigs, J. Timothy  
: REGISTRATION NUMBER: 38,241  
: REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (919) 541-8587  
: TELEFAX: (919) 541-8689  
: INFORMATION FOR SEQ ID NO: 11:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1608 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA

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FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1608
; OTHER INFORMATION: /product= "Altered form of NIM1"
; OTHER INFORMATION: /note= "c-terminal deletion compared to wild-type NIM1."
; US-08-996-685-11

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Best Local Similarity 56.8%; Pred. No. 1.7e-80;
Matches 886; Conservative 0; Mismatches 622; Indels 51; Gaps 5;

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RESULT 7
US-08-989-478-9
; Sequence 9, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 60/033,177
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1410
OTHER INFORMATION: /product= "Altered form of NIM1"
OTHER INFORMATION: /note= "N-terminal deletion compared to wild-type NIM1"
US-08-989-478-9

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Best Local Similarity 58.3%; Pred. No. 6.1e-80;
Matches 808; Conservative 0; Mismatches 548; Indels 30; Gaps 4;

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```

APPLICANT: Ryals, John  
APPLICANT: Friedrich, Leslie  
APPLICANT: Uknes, Scott  
APPLICANT: Molina, Antonio  
APPLICANT: Ruess, Wilhelm  
APPLICANT: Knauf-Beiter, Gertrude  
APPLICANT: Kung, Ruth  
APPLICANT: Kessmann, Helmut  
APPLICANT: Oostendorp, Michael  
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6031153artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No. 6031153th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/996,685  
FILING DATE:  
CLASSIFICATION:  
PRIORITY DATA:  
APPLICATION NUMBER: US 08/761,543  
FILING DATE: 6-DEC-1996  
PRIORITY DATA:  
APPLICATION NUMBER: US 60/034,378  
FILING DATE: 27-DEC-1996  
PRIORITY DATA:  
APPLICATION NUMBER: US 60/034,379  
FILING DATE: 27-DEC-1996  
PRIORITY DATA:  
APPLICATION NUMBER: US 60/034,382  
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PRIORITY DATA:  
APPLICATION NUMBER: US 60/035,024  
FILING DATE: 10-JAN-1997  
PRIORITY DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: PE/5-21215/PI/CCCL1912  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1597 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1410  
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OTHER INFORMATION: /note= "N-terminal deletion compared to wild-type NIM1"

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US-08-989-478-13  
; Sequence 13, Application US/08989478  
; Patent No. 5986082  
; GENERAL INFORMATION:  
; APPLICANT: Uknes, Scott  
; APPLICANT: Hunt, Michelle  
; APPLICANT: Steiner, Henry-York  
; APPLICANT: Ryals, John  
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING  
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5986082artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: No. 5986082th Carolina  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,478  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/033,177  
; FILING DATE: 13-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,379  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,382  
; FILING DATE: 27-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/034,730  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/035,021  
; FILING DATE: 10-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/035,022  
; FILING DATE: 10-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911  
; TELEPHONE: (919) 541-8587  
; TELEFAX: (919) 541-8689  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1194 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1194  
; OTHER INFORMATION: /product= "Altered form of NIM1"  
; OTHER INFORMATION: /note= "N-terminal/C-terminal chimera."  
; US-08-989-478-13

Query Match 19.6%; Score 400.4; DB 2; Length 1194;  
Best Local Similarity 59.8%; Pred. No. 4.4e-78;  
Matches 715; Conservative 0; Mismatches 466; Indels 15; Gaps 2;  
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RESULT 10
US-08-996-685-13
; Sequence 13, Application US/08996685
; Patent No. 6031153
; GENERAL INFORMATION:
; APPLICANT: Ryals, John
; APPLICANT: Friedrich, Leslie
; APPLICANT: Uknes, Scott
; APPLICANT: Molina, Antonio
; APPLICANT: Ruess, Wilhelm
; APPLICANT: Knaf-Belter, Gertrude
; APPLICANT: Kung, Ruth
; APPLICANT: Kessmann, Helmut
; APPLICANT: Oostendorp, Michael
; TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 6031153artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6031153th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/761,543

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; FILING DATE: 6-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,378
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,024
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/875,015
; FILING DATE: 16-JUL-1997
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1194
; OTHER INFORMATION:
; OTHER INFORMATION: /note="N-terminal/C-terminal chimera."
US-08-996-685-13

Query Match 19.6%; Score 400.4; DB 3; Length 1194;
Best local Similarity 59.8%; Pred. No. 4,4e-78;
Matches 715; Conservative 0; Mismatches 466; Indels 15; Gaps 2;

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 US-08-989-478-15  
 : Sequence 15, Application US/08989478  
 : Patent No. 5986082  
 : GENERAL INFORMATION:  
 : APPLICANT: Uknes, Scott  
 : APPLICANT: Hunt, Michelle  
 : APPLICANT: Steiner, Henry-York  
 : APPLICANT: Ryals, John  
 : TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING  
 : TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS  
 : NUMBER OF SEQUENCES: 32  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: No. 5986082artis Corporation

STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: No. 5986082th Carolina  
 COUNTRY: USA  
 ZIP: 27709  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/989,478  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/033,177  
 FILING DATE: 13-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,379  
 FILING DATE: 27-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,382  
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 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/035,022  
 FILING DATE: 10-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/035,021  
 FILING DATE: 10-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/035,022  
 FILING DATE: 10-JAN-1997  
 ATORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: PF-5-21214/P1/CGC1911  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 541-8587  
 TELEFAX: (919) 541-8689  
 INFORMATION FOR SRO ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 786 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
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 OTHER INFORMATION:  
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 Matches 456; Conservative 0; Mismatches 282; Indels 12; Gaps 1;  
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RESULT 12
US-08-996-685-15
Sequence 15, Application US/08996685
Patent No. 6031153
GENERAL INFORMATION:
APPLICANT: Ryals, John
APPLICANT: Friedrich, Leslie
APPLICANT: Uknes, Scott
APPLICANT: Molina, Antonio
APPLICANT: Ruess, Wilhelm
APPLICANT: Knauf-Belter, Gertrude
APPLICANT: Kung, Ruth
APPLICANT: Kessmann, Helmut
APPLICANT: Oostendorp, Michael
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwalis Road
CITY: Research Triangle Park
STATE: No. 6031153Ith Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM PC-DO5/MS-DO5
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/761,543
FILING DATE: 6-DEC-1996

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	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US 60/034,378	
	FILING DATE: 27-DEC-1996	
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	PRIOR APPLICATION DATA:	
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	APPLICATION NUMBER: US 60/035,024	
	FILING DATE: 10-JAN-1997	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US 08/075,015	
	FILING DATE: 16-JUL-1997	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Meigs, J. Timothy	
	REGISTRATION NUMBER: 38,241	
	REFERENCE/DOCKET NUMBER: PE/5-21215/P1/CGC1912	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (919) 541-8587	
	TELEFAX: (919) 541-8689	
	INFORMATION FOR SEQ ID NO: 15:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 786 base pairs	
	TYPY: nucleic acid	
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OY	592 gaagtataaacctctatgatcttatctatctgttcgcaactlatacaacaactcttgacg	651
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13 RESULT
14 US-08-989-478-1
15 : Sequence 1, Application US/08989478
16 : Patent No. 5986082
17 : GENERAL INFORMATION:
18 : APPLICANT: Uknes, Scott
19 : APPLICANT: Hunt, Michelle
20 : APPLICANT: Steiner, Henry-York
21 : APPLICANT: Ryals, John
22 : TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
23 : TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
24 : NUMBER OF SEQUENCES: 32
25 : CORRESPONDENCE ADDRESS:
26 : ADDRESSEE: No. 5986082artis Corporation
27 : STREET: 3054 Cornwallis Road
28 : CITY: Research Triangle Park
29 : STATE: No. 5986082th Carolina
30 : COUNTRY: USA
31 : ZIP: 27709
32 : COMPUTER READABLE FORM:
33 : MEDIUM TYPE: Floppy disk
34 : COMPUTER: IBM PC compatible
35 : OPERATING SYSTEM: PC-DOS/MS-DOS
36 : SOFTWARE: Patentln Release #1.0, Version #1.30
37 : CURRENT APPLICATION DATA:
38 : APPLICATION NUMBER: US/08/989,478
39 : FILING DATE:
40 : CLASSIFICATION:
41 : PRIOR APPLICATION DATA:
42 : APPLICATION NUMBER: US 60/033,177
43 : FILING DATE: 13-DEC-1996
44 : PRIOR APPLICATION DATA:
45 : APPLICATION NUMBER: US 60/034,379
46 : FILING DATE: 27-DEC-1996
47 : PRIOR APPLICATION DATA:
48 : APPLICATION NUMBER: US 60/034,382
49 : FILING DATE: 27-DEC-1996
50 : PRIOR APPLICATION DATA:
51 : APPLICATION NUMBER: US 60/034,730
52 : FILING DATE: 10-JAN-1997
53 : PRIOR APPLICATION DATA:
54 : APPLICATION NUMBER: US 60/035,021
55 : FILING DATE: 10-JAN-1997

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Query Match	12.7%	Score 258.4	DB 2	Length 5655
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Db	3419	TATTTCAGAGGACACTATTATTGGACGTTGTAGACAAAGTTGTTTATAGAGGACATATTGGTTA	3478	
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OY	854	tagtaagatagtgctgaactgaagacagacaaactcttgatataatgcgtttgaacgcact	913	
Db	3707	TAGTAAAGTGTGTTTGGAAAGAGATCAACCAAACTCATATATGATAGCGTGCTCTTCATTT	3766	
OY	914	acgcgcgtgaacattgtgaactccaataatcacacagagcttttgatctgcgcacttgcag	973	
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Db 3887 AGCCACAATGTATCTATCTATTGTAAGGATGCAAGTGCATGCAAGCAACTTTGG 3946
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Db 4127 AATTGAAGATGACGCTGCTGATCTTGAATAATAGAGT 4164

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## RESULT 14

US-08-996-685-1

Sequence 1, Application US/08996685

Patent No. 6031153

GENERAL INFORMATION:

APPLICANT: Ryals, John

APPLICANT: Friedlich, Leslie

APPLICANT: Uknes, Scott

APPLICANT: Molina, Antonio

APPLICANT: Ruess, Wilhelm

APPLICANT: Knauf-Belter, Gertrude

APPLICANT: Kung, Ruth

APPLICANT: Kessmann, Helmut

APPLICANT: Oostendorp, Michael

TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6031153artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: No. 6031153th Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/996,685

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/761,543

FILING DATE: 6-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,378

FILING DATE: 27-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,379

FILING DATE: 27-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,382

FILING DATE: 27-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,730

FILING DATE: 10-JAN-1997

PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21215/PI/CGC1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: exon
LOCATION: 2787..3347
OTHER INFORMATION: /product= "1st exon of NIM1"
FEATURE:
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LOCATION: 3427..4162
OTHER INFORMATION: /product= "2nd exon of NIM1"
FEATURE:
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LOCATION: 4271..4474
OTHER INFORMATION: /product= "3rd exon of NIM1"
FEATURE:
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LOCATION: 4586..4866
OTHER INFORMATION: /product= "4th exon of NIM1"
NAME/KEY: CDS
LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
US-08-996-685-1

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Query Match 12.7%; Score 258.4; DB 3; Length 5655;  
 Best Local Similarity 60.0%; Pred. No. 4,6e-47;  
 Matches 455; Conservative 0; Mismatches 291; Indels 12; Gaps 1;

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Db 3539 AGATTATGTGCAAGTCTAATGTAGATATGTTAGTTGCTTGAAGATCTTCCGGAAGAC 3598
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OY	914	aagccgtcgaaacattgctgactccaanaattacaacgaagcttttgaatctcgcgacttgag	973
Db	3767	TGCGTGTTGGCATATTGGCAATGTGAAGCCGCAACAGATCTTTTAAACCTTGAATCTTGGCG	3826
OY	974	atgttaatcatagaaacccaagaaggtatatacttcttcaacttggttggaagcgaaag	1033
Db	3827	ATGTCAACCATAGGAATCCAGGSGGATATACGGTGCTTATGTTGCTGGAGTCCGAAGG	3886
OY	1034	agcctaaatcatctgtctccctttaaaccaaggggctcgacaagaatgttataatcgy	1093
Db	3887	AGCCACATTCATCTACTATCTCTATTGGAAAAGGTGCAAGTGATCAGAACGACTTTGG	3946
OY	1094	atggggagaaaagcgggttcaattctcaaaaagctaaacaacaagaaggatcttcttggg	1155
Db	3947	AAGGTAGACCGCATATGATGATGCCAAACACCCACTATGGCGGTGATTAATTAATA	4006
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RESULT 15  
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Sequence 2, Application US/08880179  
Patent No. 6091004  
GENERAL INFORMATION:  
APPLICANT: Ryals, John  
APPLICANT: Delaney, Terry  
APPLICANT: Friedrich, Leslie  
APPLICANT: Weymann, Kristiana  
APPLICANT: Lawton, Kay  
APPLICANT: Ellis, Daniel  
APPLICANT: Uknes, Scott  
APPLICANT: Jesse, Taco  
APPLICANT: Vos, Pieter  
TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE  
TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESISTANCE  
TITLE OF INVENTION: IN PLANTS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6091004artis Corporation  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880.179  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Melgs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1909  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587

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1 TELEFAX: (919) 541-8689
2 INFORMATION FOR SEQ ID NO: 2:
3 SEQUENCE CHARACTERISTICS:
4 LENGTH: 5655 base pairs
5 TYPE: nucleic acid
6 STRANDEDNESS: single
7 TOPOLOGY: linear
8 MOLECULE TYPE: DNA (genomic)
9 HYPOTHEICAL: NO
10 ANTI-SENSE: NO
11 FEATURE:
12 NAME/KEY: exon
13 LOCATION: 2787..3347
14 OTHER INFORMATION: /product= "1st exon of NIM1"
15 FEATURE:
16 NAME/KEY: exon
17 LOCATION: 3427..4162
18 OTHER INFORMATION: /product= "2nd exon of NIM1"
19 FEATURE:
20 NAME/KEY: exon
21 LOCATION: 4271..4474
22 OTHER INFORMATION: /product= "3rd exon of NIM1"
23 FEATURE:
24 NAME/KEY: exon
25 LOCATION: 4586..4866
26 OTHER INFORMATION: /product= "4th exon of NIM1"
27 FEATURE:
28 NAME/KEY: CDS
29 LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
30 US-08-860-179-2

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QY	674	ataatgtagtcgcggccaacaccttgacatgatattaccctcttgagaagatcatgcctccagatg	733					
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QY	734	ttatcaacagatatttgatgacgcacctaaagccctgcattaaatttcaccagaaaaaagg	793					
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QY	854	tatcagaagatcgtcctcactgaagagacagacaacacttgatgatgcgtttgacacgcact	913					
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QY	1034	agccataaactatgtccctctttaaaccagaaggggcgcgaaccagatgttacaatcgc	1093					
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Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 2040

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Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2020.8	99.1	2194	21 AAA61047	Rice putative nega
3	590.2	28.9	1731	21 AAA97191	L. esculentum NIM1
4	563.4	27.6	1767	21 AAA97190	N. tabacum NIM1 ho
5	556.8	27.3	2172	19 AAV16852	Nicotiana glutinos
6	556.8	27.3	2299	21 AAA97229	B. vulgaris NIM1 h
7	422.2	20.7	2024	21 AAC37765	Arabidopsis thalia
8	422.2	20.7	2104	19 AAV16851	Arabidopsis thalia
9	420.6	20.6	2011	19 AAV46274	A. thaliana NIM-1
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22	344.2	16.9	659	21 AAA97211	N. tabacum NIM1 ho
23	317.2	15.5	2069	21 AAA61048	Rice putative nega
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29	309.8	15.2	2120	22 AAC84345	Wheat Nph2-2 cDNA
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34	265.4	13.0	2844	21 AAA97230	H. annuus NIM1 homo
35	264.8	13.0	786	19 AAV46279	A. thaliana NIM-1
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37	262	12.8	1761	21 AAA97193	A. thaliana NIM1 h
38	260.4	12.8	2171	21 AAC46895	Arabidopsis thalia
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#### ALIGNMENTS

RESULT 1	
ID AAC81457	standard; cDNA; 2040 BP.
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AC AAC81457;	
XX	
DT 28-FEB-2001	(first entry)
XX	
DE Rice NPR1 homologue 1 (NIM1) cDNA, SEQ ID NO:3.	
XX	
KW Rice; NIM1; NPR1 homologue 1; PNI interactor; SAR; bZIP protein;	
KW systemic acquired resistance; Yeast two-hybrid system; transgenic plant;	
KW pathogen resistance; virus; bacterium; nematode; fungus; insect; ss.	
XX	
OS Oryza sativa.	
XX	
PN WO200063417-A2.	
XX	
PD 26-OCT-2000.	
XX	
PF 06-APR-2000; 2000WO-US09060.	
XX	
PR 19-APR-1999; 99US-0294539.	
XX	
PA (REGC ) UNIV CALIFORNIA.	
XX	
PI Chern MS, Ronald P;	
XX	
DR WPI: 2001-090867/10.	
DR P-PSDB; AAB29750.	
XX	
PT Novel nucleic acid construct for enhancing pathogen resistance, encodes	
PT rice proline rich NPR1 interactor proteins, polypeptides interacting	
PT with PNI or NIM1, and bZIP protein interacting with Arabidopsis NPR1	



OY	1681	aatgcgaagctcgagggtccttcgctgctgctacatgcacatcgctggccattcgacca	1740
OY	1681	aatgcgaagctcgagggtccttcgctgctgctacatgcacatcgctggccattcgacca	1740
Db	1681	aatgcgaagctcgagggtccttcgctgctgctacatgcacatcgctggccattcgacca	1740
OY	1741	aggagaatgaaccaccttgcctcccacaataagtgcacatatgatagctactgcctctg	1800
Db	1741	aggagaatgaaccaccttgcctcccacaataagtgcacatatgatagctactgcctctg	1800
OY	1801	agctactcaccttgatggtttgctctctgtcaattgccccccaataatatctcattggtt	1860
Db	1801	agctactcaccttgatggtttgctctctgtcaattgccccccaataatatctcattggtt	1860
OY	1861	aggcttgtcacatgattagttcttacacgcatcttgcgccgctaattgtgaaacgcagaagt	1920
Db	1861	aggcttgtcacatgattagttcttacacgcatcttgcgccgctaattgtgaaacgcagaagt	1920
OY	1921	tcaactagtctgttactcagagtgtaataacaagtgccttgattgttgattgttgaa	1980
Db	1921	tcaactagtctgttactcagagtgtaataacaagtgccttgattgttgattgttgaa	1980
OY	1981	tttccagtggttctgctcgtcaaaaaatgagatgattcttggcaaaaaaaaaaaaaaaa	2040
Db	1981	tttccagtggttctgctcgtcaaaaaatgagatgattcttggcaaaaaaaaaaaaaaaa	2040

RESULT 2

AAAG61047	standard; cDNA; 2194 BP.
AC	AAA61047;
XX	12-OCT-2000 (first entry)
DE	Rice putative negatively phytochrome regulated 1 (NPR1) gene #1.
XX	
KW	Rice: negatively phytochrome regulated 1 gene; NPR1:
KN	systemic acquired resistance; gene mapping; transgenic plant; ss.
XX	
OS	Oryza sativa.
XX	
FH	Key Location/Qualifiers
FT	CDS 140..1876
ET	/tag= a
FT	/product= "NPR1"
XX	
PN	WO20028036-A2.
XX	
PD	18-MAY-2000.
XX	
XX	04-NOV-1999; 99WO-US25953.
PF	
XX	
PR	05-NOV-1998; 98US-0107242.
XX	
RPA	(DUPO ) DU PONT DE NEMOURS & CO E I.
XX	
P1	Famodu OO, Fang Y, Liu Z, Miao G, Odeh JT;
DR	MPI: 2000-451636/39.
XX	
DR	P-PSDB; AAB09875.
PT	Isolated nucleic acid fragments encoding an NPR1 gene which can be used
XX	to transform plants and provide disease resistance -
PS	Claim 2; Page 29; 35pp; English.

The present sequence is a putative version of the rice negatively phytochrome regulated 1 (NPR1) gene coding sequence. It was isolated by screening a leaf cDNA library for those sequences which were involved in systemic acquired resistance and this gene can be used to create transgenic plants which are protected from pathogens. It can also be used to find homologous sequences in other plants which have a similar effect.

[illegible]

Db	1088	ctcgacacttgagatgttaatctatagaaccccaagggttatacttgcttcttaactgct	1147
Qy	1021	ggcggagggaagagagcctaataatctgtctcccttttaaccaagggtctgcaccaca	1080
Db	1148	gcggaggcgaagaagagccctaaatacatctgtctcccttttaaccaagggtctgcaccaca	1207
Qy	1081	gagcttcaatcgcgtatggaagaagaagcgtgttcaaatctcaaaaaagcctaacaagaag	1140
Db	1208	gagcttcaatcgcgtatggaagaagaagcgtgttcaaatctcaaaaaagcctaacaagaag	1267
Qy	1141	gattactttggtgttaccggaagaagaaacctctcccaaaagatagtagttatgttaa	1200
Db	1268	gattactttggtgttaccggaagaagaaacctctcccaaaagatagtagttatgttaa	1327
Qy	1201	atacttggagcaagctctgnaaaaagggccccacaactcgggaagagcactcaattctcttga	1260
Db	1328	atacttggagcaagctctgnaaaaagggccccacaactcgggaagagcactcaattctcttga	1387
Qy	1261	atggcagagtgaagatctacagaggaaggttgctgtatccttgaaaccgagttgcttggca	1320
Db	1388	atggcagagtgaagatctacagaggaaggttgctgtatccttgaaaccgagttgcttggcg	1447
Qy	1321	aggagtatgttcccgatggcgagggcgcaagatagacaatgatatgtgtccaaatgtgaatgaact	1380
Db	1448	aggagtatgttcccgatggcgagggcgcaagatagacaatgatatgtgtccaaatgtgaatgaact	1507
Qy	1381	tttgaaattcaacctggtgtctctggttgcaaaatccacacctctctgnaaagaacaacggacaactgtt	1440
Db	1508	tttgaaattcaacctggtgtctctggttgcaaaatccacacctctctgnaaagaacaacggacaactgtt	1567
Qy	1441	gattctaataagaagtcctcttccataatgaagaagaacacttgctccggatgtgacagcactc	1500
Db	1568	gattctaataagaagtcctcttccataatgaagaagaacacttgctccggatgtgacagcactc	1627
Qy	1501	tcccaaacagtgtagcgtccggagaaacgcttttcccgcgatgttcgaaacgtgtgcacag	1560
Db	1628	tcccaaacagtgtagcgtccggagaaacgcttttcccgcgatgttcgaaacgtgtgcacag	1687
Qy	1551	atcatatgatgatgaactgatccggcttccctctcgagaagacacgtccggcggagaagag	1620
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Qy	1621	aagaggttctcatgacctgcgcagagatgttcttccagaagaagcatccacgagagacaagaagag	1680
Db	1748	aagaggttctcatgacctgcgcagagatgttcttccagaagaagcatccacgagagacaagaagag	1807
Qy	1661	aatgacaggttcgggggtcctcgtcgtcgtcgtcgtcatcgacaatcgatccggggccattcgacca	1740
Db	1808	aatgacaggttcgggggtcctcgtcgtcgtcgtcgtcatcgacaatcgatccggggccattcgacca	1867
Qy	1741	aggagatgaacaacattgtgtccccaataatgttgcattgatgatgaatgaatgtgtccctccgg	1800
Db	1868	aggagatgaacaacattgtgtccccaataatgttgcattgatgatgaatgaatgtgtccctccgg	1927
Qy	1801	agctactcacctgtagtgttgcctctgtcattgcatgtccccccaataatatctctaactgtgtt	1860
Db	1928	agctactcacctgtagtgttgcctctgtcattgcatgtccccccaataatatctctaactgtgtt	1987
Qy	1861	aggcttgtacaagtatattagttcttacaagctattgccccgtccaattgtgaaacgcagaagtc	1920
Db	1988	aggcttgtacaagtatattagttcttacaagctattgccccgtccaattgtgaaacgcagaagtc	2047
Qy	1921	tcatctagtgctgttaacctgcggaggtgtataaagaatgtttgaattgtgaagtgtactgtgaa	1980
Db	2048	tcatctagtgctgttaacctgcggaggtgtataaagaatgtttgaattgtgaagtgtactgtgaa	2107
Qy	1981	tttccagatggtttgtctcgttaaaaaatgagatgatatcttgcgcataaaaaaataaaaaaaa	2040
Db	2108	tttccagatggtttgtctcgttaaaaaatgagatgatatcttgcgcataaaaaaataaaaaaaa	2167

[illegible]

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Db 428 ctgttaggcagcgtgtggtcccttcattgttcagggtttgtgacgcatcccttacccttcaga 487
Qy 536 tcgcgcagctccaccaaccttccagcggtctccttgatctccttgataaagttgaag 555
Db 488 tccctcaatgtgcgaagaattccagagacacattgtatcttctgacaagaactgtag 547
Qy 596 tagataacctctattgattctgttcgttcgaactatgacaacaactctgtatgaac 655
Db 548 caatgatgtatgattggtttatccgttcgaacatttcggttaagcattgtgaagat 607
Qy 656 tgccttgaagaatgcttgatattgtatgtccgttcgaacaccttcgaatgattacattaga 715
Db 608 tacttcaagaatgattgattattgttcaagctaaagtgttatcatatacacttgata 667
Qy 716 agtcatgctcccaagatgtatatacaagacattttagtcagcgcctaaagcctcgattaa 775
Db 668 agtctctgctccatgtacattgtataaacaatacactgtacgtgctgacttgcgtgc 727
Qy 776 ttccacagagaacaaggggttccctcaacaacatgtgagagatatacagaagccttg 835
Db 728 aaggccttgagaagaatggtttccctgataaacaatgttaagagatacatagagcattg 787
Qy 836 actctgacgatgtagagctagtcaggaggtctgtcactgtagaagacagacaacattgagt 895
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Db 848 atgcatatgctcccaactatgctgttagcatattgcgtacagtgacaagactacagcagaactt 907
Qy 956 tggatctgcacttgacgatgttaatacatagaaacccaagaagttatactgtcttcaca 1015
Db 908 tagatcttcaactgtctgattgattatcatcaaatccctgaagagacacagcttactcatg 967
Qy 1016 ttctctgagagcggaagagccttaaaatcatgtctccctttaaaccgaaggggctgcag 1075
Db 968 ttgctgcacatgaggaagaacccaataattatagtgccctttaaaccgaagggcctagag 1027
Qy 1076 cagcagatgttatactcgatgtgagagaagaagcggttcaaatlccaaagaactacaac 1135
Db 1028 ctctgactcgacatccgatgtgcacaaagaacacttcaattgttaagaggtctactagcg 1087
Qy 1136 aaggagattacttgggtgttaccggaagaagaaccttccaaaagaagttatgta 1195
Db 1088 ttgtagattttacaaagctcacagaggaagaatctgtctcaaaagagtcggttattgca 1147
Qy 1196 ttgaatactgagcgaagctgaaagaagaggaagcgaacactcgaggaagcactgattctc 1255
Db 1148 ttgagattctgagcgaagcgaagaagaagagatccactactacaggaagcttcatatctc 1207
Qy 1256 ttgcaatgacaggttgaagctctacagaggaaggttgcgtatcttgaacacaggttgc 1315
Db 1208 ttgctatgtagagcgatgttgcgtatgtaagctgttatcccttgaataaagagttggtc 1267
Qy 1316 ttgcaagaggtatggttcogattgagcgaagaatgaagatgaagttatgtcccaagttgatg 1375
Db 1268 ttgctaaacaccttltcccatgtgaagcaaaagtgtcaatgagacatgacacaaagtgtatg 1327
Qy 1376 gaacttgaatttaacctgtggtctggtgctgacatccactcctctgaaagaacagacaa 1435
Db 1328 gacgcgtctgaattaccctcggtctagcatgaggaagaagatagctgtgacagaagaacaa 1387
Qy 1436 ctgtgtatcctaataatgaagctcttcataatgaagaagaacacttagctcgatgacag 1495
Db 1388 cagttgatttgaacgagcgctcttcaagatgaagagagcacttgaactcgctttaggg 1447
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Qy 1556 acaagaatcatgtgattgta-----aactgacgcggttccctcgggaagagacgctccg 1609

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Db 1508 ataagatcatgattgctgattgactgtctgtgatatgattacatgaggggaatgacagtag 1567
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Db 1568 aagagcgtcaactgaaagaagaagatgacatggaacttcaagaatattgttctcaagcat 1627
Qy 1661 tccagagaggaaggaaggaatgacaggtgcgggctcgtgtgtgtgtgtgtgtgtgtgtgtgt 1720
Db 1628 tccagagaggaataaagaagaattgtctaagactaacatgltccatctgttctccatcat 1687
Qy 1721 cgatcgagg 1729
Db 1688 ctaaggag 1696

RESULT 4
AAA97190
ID AAA97190 standard; cDNA; 1767 BP.
XX
AC AAA97190:
XX
DT 25-JAN-2001 (first entry)
XX
DE N. tabacum NIM1 homologue coding sequence SEQ ID NO: 1.
XX
KW Systemic acquired resistance; SAR; signal transduction cascade;
KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
KW potato; ss.
XX
OS Nicotiana tabacum.
XX
FH key
FT 1..1767
FT CDS /tag= a
FT /product= "NIM1 homologue"
XX
PN MO200053762-A2.
XX
PD 14-SEP-2000.
XX
PF 07-MAR-2000; 2000WO-EP01978.
XX
PR 09-MAR-1999; 99US-0265149.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Salmeron JM, Weislo LJ, Willits MG, Mengiste T;
XX
DR WPI; 2000-594322/56.
XX
DR P-PDB; AAB27301.
XX
PT Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are
PT homologues of Arabidopsis NIM1 gene -
XX
PS Claim 3; Page 68-70; 152pp; English.
XX
CC The present invention is concerned with the isolation of NIM1 homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC gene and protein can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidogyne incognita. In particular they can be used against disease
CC organisms of maize.
XX

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XX 17-OCT-2000 (first entry)
DT Arabidopsis thaliana DNA fragment SEQ ID NO: 18587.
XX
DE Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 26-AUG-1999; 99US-0150884.
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 QY 1393 ctg---ggtctgtgtgcaaatccacctccctgaaagacaaggaactgtgtactaat 1449  
 Db 1414 gtactagctctgagctgacgtctcactgtgtacgaagaacatcacgggtgttaaag 1473  
 QY 1450 gaagatctctcaatgaagaagaaacacttagctcgtgtgacagcaactcccaaca 1509  
 Db 1474 atgcacctctcgaatccctcagaagaacacaaagtactaaagcgtttcctaacc 1533  
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 QY 1567 ---gagtgaactgctgctcgtttccctcgtggaagaaacgttcggtg-----gag 1614  
 Db 1594 tgtgagactgactgactcactcgtgtcggaagaacgactgtgtgaaacgactaca 1653  
 QY 1615 aagaaggaaggtttcactcgtcgaagatgttctcgaagaagcattccacgaagacaag 1674  
 Db 1654 aagaagcaaggtacatggaatacagaagacactaaagaagcctttagtgagacaat 1713  
 QY 1675 gaagagaatgacaggttcggtgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1734  
 Db 1714 ttggaattggaattcgtccctcgaagattcgacttcgtcgtcgtcgtcgtcgtcgtcgt 1773  
 QY 1735 cgaccgaag 1743  
 Db 1774 ggaagaagag 1782

RESULT 8  
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 ID AAV16851 standard; cDNA; 2104 BP.  
 AC AAV16851;  
 DT 17-AUG-1998 (first entry)  
 DE Arabidopsis thaliana acquired resistance gene NPR1.  
 KW NPR1 gene; acquired resistance; disease; plant pathogens; bacteria;  
 KM mycoplasma; fungi; insects; nematodes; viruses; viroids;  
 XX transgenic; ds.  
 OS Arabidopsis thaliana.  
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 FT /note= NPR1 gene  
 FT /note= resistance protein  
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 PN MO9806748-A1.  
 PD 19-FEB-1998.  
 PF 08-AUG-1997; 97MO-US13994.  
 PR 16-MAY-1997; 97US-0046769.  
 PR 09-AUG-1996; 96US-0023851.  
 PR 10-JUN-1997; 97US-0035166.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (UYDU-) UNIV DUKE.  
 PI Ausubel FM, Cao H, Dong X, Glazebrook J;  
 DR WPI, 1998-159458/14.  
 DR P-PSDB; AAW46940.  
 PT New isolated plant acquired resistance polypeptide gene - useful  
 PT for, e.g. producing plants with increased resistance to pathogens

PT such as bacteria  
 XX Claim 9; Fig 5; 127pp; English.  
 PS The sequence is that of the acquired resistance gene NPR1. It may be  
 CC used in the production of transgenic cells which can produce the encoded  
 CC acquired resistance protein. Such transgenic plants cells are  
 CC useful in the production of plants having an increased level  
 CC of resistance against disease caused by plant pathogens, e.g.  
 CC bacteria, mycoplasmas, fungi, insects, nematodes, viruses,  
 CC and viroids.  
 XX Sequence 2104 BP; 606 A; 431 C; 482 G; 585 T; 0 other;  
 SQ

Query Match 20.7%; Score 422.2; DB 19; Length 2104;  
 Best Local Similarity 56.0%; Pred. No. 9.3e-62;  
 Matches 980; Conservative 0; Mismatches 703; Indels 66; Gaps 7;

QY 13 accgacagctcaccaagcgttctcgtactcgagacgagcgttcgtgaggaaggagac 72  
 Db 141 actagttcgtcgtaccgataacacgactcctctatgttactgtgcccgaacaa 200  
 QY 73 gccgacgagacgagcagctggaagcgtccgcgctctccgaacactcgcgcgagc 132  
 Db 201 gtactcaacgagactgtatgtatctcgtcgtcaattgtcttcaacagcttcgaatcgtc 260  
 QY 133 ttcgcctgcgcgagactcgtctcctcgcgacgagcgcgtccgtccgagcgcgc 192  
 Db 261 tttagctgcgcgagatttc-----tacagcagcgttaagcttgtt 302  
 QY 193 ggcgcgagc 252  
 Db 303 ctcccgacgagc 362  
 QY 253 ctgc 312  
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 QY 313 agcgaagagctgagcgtccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 372  
 Db 417 gccgtgaagctcgc 464  
 QY 373 tagcagc 432  
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 QY 433 aagcgcgcgtcgtcgtcgc 492  
 Db 525 aaagaggttctgtaagtgc 584  
 QY 493 gcgtcagtgccgc 552  
 Db 585 gattcagtggtgaggtgtcttattgttgcttcaatcgaagccgcgcgcgcgcgcgcgcgc 644  
 QY 553 ctctccagc 612  
 Db 645 ctctcagagagcacttattgagcgttgtagacaaggtgttagagagacacattggtt 704  
 QY 613 attctatcgttgcgaacttgcgaacaaactcgtcgaagcgcgcgcgcgcgcgcgcgcgcgc 672  
 Db 705 atactcaagcctcgtcgaataatgtgtaaaagcgttgtagaagcattggaagatgtaaa 764  
 QY 673 gatagttagtcgtcgaacacttgcgaatgtaactcttgaagcgcgcgcgcgcgcgcgcgcgc 732  
 Db 765 gagattatgtcaagctcaatgtagatagattgttgcgttgaagcgcgcgcgcgcgcgcgcgc 824  
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 Db 825 ctgttaagagataatgtagc 884  
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DB 933 ttatgaatgtctgtcttgaaagagatcacacacacatctatgatgtgctgtctctac 992
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DB 993 ttcgcgtgtgtcattgtcattgtgaagaccgacacacatctttaaactatgatcttgc 1052
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QY 1675 gaagagaatcacagcgtcggcggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1734
DB 1773 tctggaatgaagaatctcgtcctcgtcgaagatctcgtcgtcgtcgtcgtcgtcgt 1832
QY 1735 cgaccaaag 1743
DB 1833 ggaagaagag 1841

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RESULT 9
AAV46274
ID AAV46274 standard; cDNA; 2011 BP.
XX
AC AAV46274;
XX

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DT 16-OCT-1998 (first entry)
XX
DE A. thaliana NIM-1 cDNA.
XX
KW NIM-1; noninducible immunity; systemic acquired resistance; SAR;
KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 43..1824
FT /tag=a
FT /product=NIM-1
XX
XX W09829537-A2.
XX
XX 09-JUL-1998.
XX
XX 23-DEC-1997; 97WO-EP07253.
XX
XX 10-JAN-1997; 97US-0035024.
XX
XX 27-DEC-1996; 96US-0034378.
XX
XX (NOVS ) NOVARTIS AG.
XX
PI Friedrich LB, Molina Fernandez A, Ryals JA, Uknes SJ;
XX
XX WPI: 1998-388119/33.
XX
XX P-PSDB: AAW64435.
XX
PT Protection of immunomodulated plants against pathogens - comprises
PT applying microbicide to provide increase in resistance
XX
PS Disclosure: Page 112-115; 164pp; English.
XX
XX
XX This cDNA sequence encodes the NIM-1 protein from Arabidopsis thaliana.
XX This protein is used in a method resulting in the protection of an
XX immunomodulated plant having a first level of resistance and involves
XX treatment with at least 1 microbicide that confers a second level of
XX resistance, such that the plants have a third level of resistance greater
XX than the sum of the first two levels. The method can be applied to a wide
XX variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
XX against viruses, fungi, bacteria, insects and nematodes. The method
XX provides a high level of resistance and allows a reduction in the amount
XX of microbicide used. Since the process involves two different methods of
XX protection, it is unlikely that the pathogen will develop resistance to
XX the treatment.
XX
XX Sequence 2011 BP; 563 A; 417 C; 472 G; 559 T; 0 other;
SQ

```

```

Query Match 20.6%; Score 420.6; DB 19; Length 2011;
Best Local Similarity 56.0%; Pred. No. 1.7e-61;
Matches 979; Conservative 0; Mismatches 704; Indels 66; Gaps 7;

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DB 91 actagttcgtctacgataacacgcactctctatgttatcttgccgcggaaca 150
QY 73 gccgaagcggagcgcagctgtgagggcgctcgcgcgctctccgaacactcgcggcg 132
DB 151 gtactaccggacttattgtatctgtcgaattgtctccacagctcgaatcgtc 210
QY 133 ttcgcgtcgcggagactcgtctcctcgcgcagcgcgcatacgcgtcccgaggcg 192
DB 211 ttgtaactcgcggtatcttcc-----tacgcgacgtctaagctgtt 252
QY 193 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 252
DB 253 ctctcgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 312
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Db 313 ttaagagcgcttlaag-----cgccgctaagaagagagaaagactccaacaacacggcc 366  
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 Db 367 gccgttaagctcgagcttaagagagat-----tgccaagattacagagctcg 414  
 Qy 373 taagagcgctgagctggtgctgcgaactcctacagcgccgctcgagccgccc 432  
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 Qy 553 ccttcacagcggtctcctctgactgctcctgaaggttgaagtagatacctctatg 612  
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 Db 1663 aagaagcaagagatgacatggaataacaaagacactaaagaagcctttagtgaagacaat 1722  
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 Db 1723 ttggaattgaatattgtctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1782  
 Qy 1735 cgaccaaag 1743  
 Db 1783 ggaagaag 1791

## RESULT 10

AAV46275 standard; cDNA; 2011 BP.

AAV46275;

16-OCT-1998 (first entry)

A. thaliana NIM-1 cDNA variant #1.

NIM-1: noninducible immunity; systemic acquired resistance; SAR;  
 pathogen: disease; protection: immunomodulated; plant: cereal; fruit:  
 vegetable; virus: fungi; bacteria; insect; nematode; microbicide; ss.

Arabidopsis thaliana.  
 OS Synthetic.

Key Location/Qualifiers  
 CDS 43..1824

FT /tag= a  
 FT /product= NIM-1  
 FT /note= "variant"  
 FT 205..207

FT mutation  
 FT /tag= b  
 FT /note= "wild type TCC is replaced by GCC"  
 FT 217..219

FT mutation  
 FT /tag= c  
 FT /note= "wild type TCG is replaced by GCG"

WO9829537-A2.

09-JUL-1998.

23-DEC-1997; 97WO-EP07253.

10-JAN-1997; 97US-0035024.

27-DEC-1996; 96US-0034378.

(NOVS ) NOVARTIS AG.

Friedrich IB, Molina Fernandez A, Ryals JA, Uknes SJ;  
 PI XX



Db 1783 ggaagagag 1791

RESULT 11

AAV43661

ID AAV43661 standard; CDNA; 2011 BP.

XX AAV43661;

AC AAV43661;

XX 29-SEP-1998 (first entry)

XX Non-inducible immunity-1 (NIM1) protein variant 1 encoding cDNA.

XX Non-inducible immunity-1 gene; NIM1 gene; disease resistance; mutant;

KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;

KW constitutive immunity; agriculture; variant; ss.

XX Arabidopsis thaliana.

OS Synthetic.

XX Key Location/Qualifiers

XX CDS 43..1824

FT /tag- a

FT /product- "NIM1 protein variant 1"

FT mutation 205..207

FT /tag- b

FT /note- "wild type TGC is replaced by GCC"

FT mutation 217..219

FT /tag- c

FT /note- "wild type TCG is replaced by GCG"

XX WO9826082-A1.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-EP07012.

XX 20-JUN-1997; 97US-0880179.

PR 13-DEC-1996; 96US-0033177.

PR 27-DEC-1996; 96US-0034379.

PR 10-DEC-1996; 96US-0034382.

PR 10-JAN-1997; 97US-0034730.

PR 10-JAN-1997; 97US-0035021.

PR 10-JAN-1997; 97US-0035022.

XX (NOVS) NOVARTIS AG.

XX Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;

PI Uknes SJ;

XX P-PDB; AAW61983.

DR WPI; 1998-348536/30.

XX Use of non-inducible immunity-1 gene - for transforming plants to

PT produce transgenic plants having a broad spectrum disease resistance

XX Claim 5; Pages 140-144; 205pp; English.

XX This cDNA encodes an altered form of the Arabidopsis thaliana non-

CC inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to

CC AAV43665 represent variants of the NIM1 cDNA. The invention provides a

CC chimeric gene comprising a promoter active in plants operatively linked

CC to a DNA molecule that encodes an altered form of the NIM1 protein. Plant

CC cells stably transformed with a recombinant vector comprising such a

CC chimeric gene have a broad spectrum of disease resistance. The altered

CC NIM1 proteins act as dominant-negative regulators of the systemic

CC acquired resistance (SAR) signal transduction pathway. The transgenic

CC plants transformed with an altered NIM1 gene exhibits constitutive SAR

CC expression which is higher in the transformed plants than in a wild-type

CC plant. The products can be used for producing plants with a broad

CC spectrum disease resistance. Overexpression of NIM1 mimics the effects

CC of inducer compounds that induce constitutive immunity (CIM) phenotype

CC in plants. The inventions can be used with plants such as rice, wheat,

CC barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea,

CC chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish,

CC spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot,

CC squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum,

CC cherry, peach, nectarine, apricot, strawberry, grape, raspberry,

CC blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco,

CC tomato, sorghum and sugarcane. The plants produced are resistant to

CC plant pathogens such as viruses, viroids, fungi, bacteria, insects such

CC as aphids and lepidoptera and nematodes. The plants produced can be used

CC in agriculture.

XX

XX Sequence 2011 BP; 563 A; 417 C; 474 G; 557 T; 0 other;

XX

Query Match 20.6%; Score 420.6; DB 19; Length 2011;

Best Local Similarity 56.0%; Pred. No. 1,7e-61;

Matches 979; Conservative 0; Mismatches 704; Indels 66; Gaps 7;

QY 13 accagcagctaccacagcgtcttcgcgactcgacagcgctcgtgagggagggac 72

DB 91 actagctcgtcgtaccgataaacacgactcctctatgtttatctggtccgcgaacaa 150

QY 73 ggcgacgagcagcagcagctgagagcgctccgcgctctccgacacacgcgcgcg 132

DB 151 gtactcaacgagcctgtatctcgtctcgtgaattgtctccacacagcttcgaagcgtc 210

QY 133 ttcgcgtccgcgagcactcgtcttcgcgcgacgcgcgcgtccgtccgcgcgcgc 192

DB 211 tttagcgcgcgcgagtgttc-----tacagcgacgactgaactgtt 252

QY 193 ggc 252

DB 253 ctctccagc 312

QY 253 ctgc 312

DB 313 ttcaagagcgcgtttac-----gcgcgtaagagaggaagaccccaacacacgcgc 366

QY 313 agcgaagagcgtgagctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 372

DB 367 gccgtgagcgtcgc 414

QY 373 tagcagc 432

DB 415 ttcgattcgcgttgcgttcttgcgttcttgcgttcttgcgttcttgcgttcttgcgtt 474

QY 433 aagc 492

DB 475 aaagaggttcttgatgagtcgacgagagatgctgcgcgcgcgcgcgcgcgcgcgcgcgc 534

QY 493 ggcgttcagtcgc 552

DB 535 gatttcattgtgaggttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 594

QY 553 ctcttcacgc 612

DB 595 ctcttcacgc 654

QY 613 attctatcgttgcacacttaac 672

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QY 793 ggaattcttaacaacatgtgagagataacacagacgccttgcgtgacagatgataag 852

DB 835 -----aaacatgctcgaatgataacataagcacttgctgagatgattgag 882

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QY 853 cgaatcagatgctcctcaatgaagacagacaatcttgatgagctgttgcactgcac 912
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QY 1615 aagaagaaagaggttcatatgacctgcagagatgtcttcagaagagcatctcagaagacaag 1674
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RESULT 12
AAVA6277
ID AAVA6277 standard: cDNA: 1608 BP.
AC AAVA6277;
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XX 16-OCT-1998 (first entry)
DT

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XX A. thaliana C-terminal truncated NIM-1 variant cDNA.
DE
XX NIM-1; noninducible immunity; systemic acquired resistance; SAR;
KW pathogen; disease; protection; immunomodulated; plant; cereal; fruit;
KW vegetable; virus; fungi; bacteria; insect; nematode; microbicide; ss.
XX
OS Arabidopsis thaliana.
XX Synthetic.
FH Key Location/Qualifiers
FT CDS 43..1608
FT /tag= a
FT /product= NIM-1
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FN W09829537-A2.
XX
PD 09-JUL-1998.
XX
XX 23-DEC-1997; 97WO-EP07253.
XX
PR 10-JAN-1997; 97US-0035024.
PR 27-DEC-1996; 96US-0034378.
XX
XX (NOVS ) NOVARTIS AG.
XX
PI Friedrich IB, Molina Fernandez A, Ryals JA, Uknes SJ;
XX WPI: 1998-388119/33.
XX DR P-PSDB: AAM64438.
XX
PT Protection of immunomodulated plants against pathogens - comprises
PT applying microbicide to provide increase in resistance
XX
PS Claim 17; Page 129-132; 164pp; English.
XX
XX This sequence encodes a truncated variant NIM-1 protein from Arabidopsis
XX thaliana. This protein is used in a method resulting in the protection of
XX an immunomodulated plant having a first level of resistance and involves
XX treatment with at least 1 microbicide that confers a second level of
XX resistance, such that the plants have a third level of resistance greater
XX than the sum of the first two levels. The method can be applied to a wide
XX variety of plants (cereals, fruits, oilseeds, vegetables etc.) to protect
XX against viruses, fungi, bacteria, insects and nematodes. The method
XX provides a high level of resistance and allows a reduction in the amount
XX of microbicide used. Since the process involves two different methods of
XX protection, it is unlikely that the pathogen will develop resistance to
XX the treatment.
SQ
Sequence 1608 BP; 447 A; 340 C; 385 G; 436 T; 0 other:

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Query Match 20.2%; Score 411.8; DB 19; Length 1608;
Best Local Similarity 56.8%; Pred. No. 4.8e-60;
Matches 886; Conservative 0; Mismatches 622; Indels 51; Gaps 5;

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DB 151 gtactacgcgacctgtagtaltctgtcgaattgtctcacaacagctcgaatccgctc 210
QY 133 ttcgctgcgcgagagactcgcgttctcctcgcgcgacgcgcgcatgcgtcccgagcgc 192
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QY 193 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 252
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Qy 433 aagagcgcgctgctcgctcgacagagactcgcccaagctcggtgtgaccccgcgctc 492
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RESULT 13
AAV43663
ID AAV43663 standard; cDNA; 1608 BP.
XX
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AC AAV43663;
XX
XX
DT 29-SEP-1998 (first entry)
XX
XX
DE Non-inducible immunity-1 (NIMI) protein variant 3 encoding cDNA.
KW Non-inducible immunity-1 gene; NIMI gene; disease resistance; mutant;
KW transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;
KW constitutive immunity; agriculture; variant; ss.
XX
OS Arabidopsis thaliana.
XX
XX
FH Key Location/Qualifiers
FT CDS 43..1608
FT FT /*tag= a
FT FT /product= "NIMI protein variant 3"
FT FT /note= "C-terminal deletion compared to wild-type
FT FT NIMI sequence"

W09826082-A1.
PD 18-JUN-1998.
XX
PF 12-DEC-1997; 97WO-EP07012.
XX
PR 20-JUN-1997; 97US-0880179.
PR 13-DEC-1996; 96US-0033177.
PR 27-DEC-1996; 96US-0034379.
PR 27-DEC-1996; 96US-0034382.
PR 10-JAN-1997; 97US-0034730.
PR 10-JAN-1997; 97US-0035021.
PR 10-JAN-1997; 97US-0035022.
XX
PA (NOVS ) NOVARTIS AG.
XX
PI Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;
PI Uknes SJ;
XX
DR WPI; 1998-348536/30.
DR P-PSDB; AAW61985.
XX
PT Use of non-inducible immunity-1 gene - for transforming plants to
PT produce transgenic plants having a broad spectrum disease resistance
XX
PS Claim 12; Pages 155-159; 205pp; English.
XX
CC This cDNA encodes an altered form of the Arabidopsis thaliana non-
CC inducible immunity-1 (NIMI) protein. Sequences shown in AAV43661 to
CC AAV43665 represent variants of the NIMI cDNA. The invention provides a
CC chimeric gene comprising a promoter active in plants operatively linked
CC to a DNA molecule that encodes an altered form of the NIMI protein. Plant
CC cells stably transformed with a recombinant vector comprising such a
CC chimeric gene have a broad spectrum of disease resistance. The altered

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RESULT	15	
AAV43662		
ID	AAV43662	standard; cDNA; 1597 BP.
XX	AC	
XX	AAV43662:	
DT	29-SEP-1998	(first entry)
XX		
DE	Non-inducible immunity-1 (NIM1) protein variant 2 encoding cDNA.	
XX		
KM	transgenic plant; SAR; systemic acquired resistance; CIM; pathogen;	
KW	constitutive immunity; agriculture; variant; ss.	
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OS	Arabidopsis thaliana.	
XX	Synthetic.	
XX		
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PR	13-DEC-1996;	96US-0003177.
PR	27-DEC-1996;	96US-0034379.
PR	27-DEC-1996;	96US-0034382.
PR	10-JAN-1997;	97US-0034730.
PR	10-JAN-1997;	97US-0035021.
PR	10-JAN-1997;	97US-0035022.
XX		
XX	(NOVS ) NOVARTIS AG.	
PA		
XX		
XX	Friedrich LB, Hunt MD, Lawton KA, Ryals JA, Steiner HY;	
PI	UKnes SJ;	
PT	WPI: 1998-348536/30.	
XX	P-PSDB; AAM61984.	
XX		
PS	Claim 9; Pages 149-152; 205pp; English.	
XX		
CC	This cDNA encodes an altered form of the Arabidopsis thaliana non-inducible immunity-1 (NIM1) protein. Sequences shown in AAV43661 to AAV43665 represent variants of the NIM1 cDNA. The invention provides a chimeric gene comprising a promoter active in plants operatively linked to a DNA molecule that encodes an altered form of the NIM1 protein. Plants cells stably transformed with a recombinant vector comprising such a chimeric gene have a broad spectrum of disease resistance. The altered NIM1 proteins act as dominant-negative regulators of the systemic acquired resistance (SAR) signal transduction pathway. The transgenic plants transformed with an altered NIM1 gene exhibits constitutive SAR expression which is higher in the transformed plants than in a wild-type plant. The products can be used for producing plants with a broad spectrum disease resistance. Overexpression of NIM1 mimics the effects of inducer compounds that induce constitutive immunity (CIM) phenotype in plants. The inventions can be used with plants such as rice, wheat, barley, rye, corn, potato, carrot, sweet potato, sugar beet, bean, pea, chitoyo, lettuce, cabbage, cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic, eggplant, pepper, celery, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot, strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya, mango, banana, soybean, tobacco, tomato, sorghum and sugarcane. The plants produced are resistant to	

CC plant pathogens such as viruses, viroids, fungi, bacteria, insects such  
CC as aphids and lepidoptera and nematodes. The plants produced can be used  
CC in agriculture.

SQ Sequence 1597 BP; 467 A; 304 C; 381 G; 445 T; 0 other;

Query Match	20.1%	Score 409.2;	DB 19;	Length 1597;
Best Local Similarity	58.3%	Pred. No. 1.3e-59;		
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ACCESSION	U76707														
VERSION	U76707.1														
KEYWORDS	GI:1773294														
SOURCE	thale cress.														
ORGANISM	Arabidopsis thaliana														

JOURNAL Submitted (30-OCT-1996) DCMB Group, Botany, Duke University, LSRC  
Building, Research Dr., Durham, NC 27708-1000, USA

## FEATURES

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OY	1615	aaggaaggaggttccatgactcgacgtcgaagtcttcgcgaagccttcacagagacaag	1674
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DEFINITION	Sequence 6 from patent US 5986082.	PAT	07-SEP-2000
ACCESSION	AR087502		
VERSION	AR087502.1	GI:10014265	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2011)		
AUTHORS	Dukes,S.,Joseph, Hunt,M.,Deulse, Steiner,H. and Ryals,J.Andrew,		
TITLE	Altered forms of the NIM1 gene conferring disease resistance in plants		
JOURNAL FEATURES	Patent: US 5986082-A 6 16-NOV-1999;		
SOURCE	Location/Qualifiers 1..2011 "/organism="unknown"		
BASE COUNT	563 a 417 c 472 g 559 t		
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OY	313	agcgaagagctcgagctccgcgagctcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	372
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Dd	475	AAAGAGTTTTCGATTGCCACAGACGAGATTCCTGCGACGTGGCTTCCGCGCGCGGGG	534
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SQ Sequence 1767 BP; 512 A; 328 C; 434 G; 493 T; 0 other;

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DT	17-AUG-1998 (first entry)
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DE	Nicotiana glutinosa NPR1 homologue.
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KW	NPR1 gene; acquired resistance; dis-
KW	mycoplasma; fungi; insects; nematod-
KW	transgenic; homologue; ds.
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WO9806748-A1.

19-FEB-1998.  
08-AUG-1997; 97WO-US13994.  
16-MAY-1997; 97US-0046769.  
09-AUG-1996; 96US-0023851.  
10-JAN-1997; 97US-0035166.

(GEHO ) GEN HOSPITAL CORP.  
(UYDD-) UNIV DUKE.

Ausubel FM, Cao H, Dong X, Glazebrook J;

WPI; 1998-159458/14.  
P-PSDB: AAW46942.

New isolated plant acquired resistance polypeptide gene - useful for, e.g. producing plants with increased resistance to pathogens such as bacteria

Claim 10: Fig 7: 127pp: English.

XX



TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 541-8587  
 TELEFAX: (919) 541-8689  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2011 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Arabidopsis thaliana  
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 US-08-989-478-6

Query Match 20.6%; Score 420.6; DB 2; Length 2011;  
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 Matches 979; Conservative 0; Mismatches 704; Indels 66; Gaps 7;

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 OY 73 gccagcagcgagcagcgagctgagcgctccgcgcgcctccgcacacacacacacacac 132  
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ADDRESS: No. 6031153artis Corporation  
STREET: 3054 Cornwalls Road  
CITY: Research Triangle Park  
STATE: No. 6031153th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/996,685  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/761,543  
FILING DATE: 6-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/034,378  
FILING DATE: 27-DEC-1996  
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APPLICATION NUMBER: US 60/035,024  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/875,015  
FILING DATE: 16-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: P/5-21215/P1/CGC1912  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8587  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
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TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
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ORGANISM: Arabidopsis thaliana  
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LOCATION: 1..2011  
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US-08-996-685-6

Query Match 20.6%; Score 420.6; DB 3; Length 2011;  
Best Local Similarity 56.0%; Pred. No. 2,2e-82;  
Matches 979; Conservative 0; Mismatches 704; Indels 66; Gaps 7







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OY 1213 gctgaagaagagaccacaaactcgagagacatcagttctcttcgaatgaggtgag 1272
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OY 1333 ccgagagagagagagatgacatgatatctcgaagtgtgatacttgaatttaac 1392
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OY 1450 gaaagtccttcataatgaaagaacacactagctcgatgacagacactcccaaaaca 1509
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OY 1510 gtgagagctcgagaaagcttctcccgagatgtcgaaagctcgacaaagatacgt--- 1566
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OY 1567 ---gatgatgaactgacccggttccctcgcgaagaagacagtcgcg-----gag 1614
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DB 1783 GGAAGAGG 1791

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## RESULT 5

US-08-989-478-11

Sequence 11, Application US/08989478

Patent No. 5986082

GENERAL INFORMATION:

APPLICANT: Uknes, Scott

APPLICANT: Hunt, Michelle

APPLICANT: Steiner, Henry-York

APPLICANT: Ryals, John

TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESS: No. 5986082artis Corporation

STREET: 3054 Cornwalls Road

CITY: Research Triangle Park

STATE: No. 5986082th Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,478

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/033,177

FILING DATE: 13-DEC-1996

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,379
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,382
FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,730
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1608
OTHER INFORMATION: /product="Altered form of NIM1"
OTHER INFORMATION: /note="C-terminal deletion compared to wild-type NIM1."
US-08-989-478-11

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Query Match 20.2%; Score 411.8; DB 2; Length 1608;  
 Best Local Similarity 56.8%; Pred. No. 1.7e-80;  
 Matches 886; Conservative 0; Mismatches 622; Indels 51; Gaps 5;

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DB 151 GATACACCGGACGATGATATCTGCTGCAATTGCTCTCCAAAGCTTCAATCCGTC 210
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DB 211 TTGACTCCCGGATGATTTTC-----TACAGGACGCTTAAGCTTGT 252
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DB 253 CTTCTCGAGGCGCGGGAAGTTCTTTCACCGGTGCTTTCACGAGAACTCTTTC 312
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DB 313 TTCAGAGCGCTTTAGC-----CGCGCTTAAGAGAGAAAGAGACATCAACAACCGGC 366
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DB 415 TTGATTCGTTGCTGACTGTTTGGCTTATGTTTACAGCAGAGATGAGACCGCGCT 474
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RESULT 6  
US-08-996-685-11  
Sequence 11, Application US/08996685  
Patent No. 6031153  
GENERAL INFORMATION:  
APPLICANT: Ryals, John  
APPLICANT: Friedrich, Leslie  
APPLICANT: Ukes, Scott  
APPLICANT: Molina, Antonio  
APPLICANT: Ruess, Wilhelm  
APPLICANT: Knauf-Beiler, Gertrude  
APPLICANT: Kung, Ruth  
APPLICANT: Kessmann, Helmut  
APPLICANT: Oostendorp, Michael  
TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 603115artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: No 6031153th Carolina  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/996, 685  
APPLICATION NUMBER: US/08/996, 685  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/761, 543  
FILING DATE: 6-DEC-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/034, 378  
FILING DATE: 27-DEC-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/034, 379  
FILING DATE: 27-DEC-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/034, 382  
FILING DATE: 27-DEC-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/034, 730  
FILING DATE: 10-JAN-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/035, 021  
FILING DATE: 10-JAN-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/035, 022  
FILING DATE: 10-JAN-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 60/035, 024  
FILING DATE: 10-JAN-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/875, 015  
FILING DATE: 16-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38, 241  
REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8689  
TELEFAX: (919) 541-8687  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1608 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA





APPLICANT: Ryals, John  
 APPLICANT: Friedrich, Leslie  
 APPLICANT: Uknes, Scott  
 APPLICANT: Molina, Antonio  
 APPLICANT: Ruess, Wilhelm  
 APPLICANT: Knauf-Belter, Gertrude  
 APPLICANT: Kund, Ruth  
 APPLICANT: Kessmann, Helmut  
 APPLICANT: Oostendorp, Michael  
 TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
 NUMBER OF SEQUENCES: 32  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 603115artlis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: No. 6031153th Carolina  
 COUNTRY: USA  
 ZIP: 27709  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentln Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/996,685  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/761,543  
 FILING DATE: 6-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,378  
 FILING DATE: 27-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,379  
 FILING DATE: 27-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,382  
 FILING DATE: 27-DEC-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/034,730  
 FILING DATE: 10-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/035,021  
 FILING DATE: 10-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/035,022  
 FILING DATE: 10-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/035,024  
 FILING DATE: 10-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/875,015  
 FILING DATE: 16-JUL-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38, 241  
 REFERENCE/DOCKET NUMBER: PF/5-21215/P1/CGC1912  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 541-8587  
 TELEFAX: (919) 541-8689  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1597 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..1410  
 OTHER INFORMATION: /product- "Altered form of NIM1"  
 OTHER INFORMATION: /note- "N-terminal deletion compared to wild-type NIM1"

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Db 1372 AAGAG 1377

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# RESULT 9

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; Sequence 13, Application US/08989478
; Patent No. 5986082
; GENERAL INFORMATION:
; APPLICANT: Uknes, Scott
; APPLICANT: Hunt, Michelle
; APPLICANT: Steiner, Henry-York
; APPLICANT: Ryals, John
; TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5986082artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 5986082Ch Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,478
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,177
; FILING DATE: 13-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,379
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,382
; FILING DATE: 27-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,730
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 60/035,021
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/035,022
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-21214/P1/GC1911
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8687
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1194
; OTHER INFORMATION:
; OTHER INFORMATION: /note="Altered form of NIM1"
; US-08-989-478-13

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Query Match 19.6%; Score 400.4; DB 2; Length 1194;
Best Local Similarity 59.8%; Pred. No. 4.4e-78;
Matches 715; Conservative 0; Mismatches 466; Indels 15; Gaps 2;

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Qy 436 gcgagctgcctcgtcgctgacagagacgtgcacacgtcgggtgcacccgcgtcg 495
Db 64 GAGGTTTCGATGCGCAGACAGAGATTCCTGCGACGTGCTGCGCGCGGTGAT 123
Qy 496 ttcataggcaggtcccttcgcgcctccaccctccacaggtcgagctcaacaccc 555
Db 124 TTCATGTTGAGGTTCTCTATTGCTTTCATCTTCATCTTCATCTTCATCTTCATCT 183
Qy 556 ttcacagcgctcctccttcttcttcttcttcttcttcttcttcttcttcttct 615
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Db 421 -----AAACATGTCGAAATGATGATGATGATGATGATGATGATGATGATG 471
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# RESULT 10 US-08-996-685-13

: Sequence 13, Application US/08996685  
 : Patent No. 6031153

## : GENERAL INFORMATION:

: APPLICANT: Ryals, John  
 : APPLICANT: Friedrich, Leslie  
 : APPLICANT: Uknes, Scott  
 : APPLICANT: Molina, Antonio  
 : APPLICANT: Rues, Wilhelm  
 : APPLICANT: Knaut-Belter, Gertrude  
 : APPLICANT: Kung, Ruth  
 : APPLICANT: Kessmann, Helmut  
 : APPLICANT: Oostendorp, Michael  
 : TITLE OF INVENTION: METHOD FOR PROTECTING PLANTS  
 : NUMBER OF SEQUENCES: 32  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: No. 6031153artis Corporation  
 : STREET: 3054 Cornwallis Road  
 : CITY: Research Triangle Park  
 : STATE: No. 6031153th Carolina  
 : COUNTRY: USA  
 : ZIP: 27709

## : COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/996,685  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/761,543

: FILING DATE: 6-DEC-1996  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/034,378  
 : FILING DATE: 27-DEC-1996  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/034,379  
 : FILING DATE: 27-DEC-1996  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/034,382  
 : FILING DATE: 27-DEC-1996  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/034,730  
 : FILING DATE: 10-JAN-1997  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/035,021  
 : FILING DATE: 10-JAN-1997  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/035,022  
 : FILING DATE: 10-JAN-1997  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/035,024  
 : FILING DATE: 10-JAN-1997  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/875,015  
 : FILING DATE: 16-JUL-1997  
 : TELECOMMUNICATION INFORMATION:  
 : REFERENCE/DOCKET NUMBER: PF/5-21215/P1/GC1912  
 : TELEPHONE: (919) 541-8587  
 : TELEFAX: (919) 541-8689  
 : INFORMATION FOR SEQ ID NO: 13:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1194 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: CDNA  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: 1..1194  
 : OTHER INFORMATION:  
 : OTHER INFORMATION: /note="N-terminal/C-terminal chimera."  
 : US-08-996-685-13

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 Db 64 GAGATTCTGAATGCGCAACAGAGATGCTCCACGTCGCTTGGCGCGGGGGTGAAT 123  
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D	364	GTTTAAAGATTAATTGATATACACTTAAAGAGCTTGGTGGAGGTACCTTAAAGTAAAG--	420
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D	652	CCACAATGTGATACATCTCTATTGGAAAAAGGCGCAAGCATCAGAAACAACCTTTGGA	711
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O	1216	gaagaaggagcccaacaacccgcgaagaagatcgaagttcttccttgcaatgcaagtgtagt	1275
D	832	GACAAACGAGAACAAATTCCTAGAGATGTTCCCTCTTTTGCACTGGCGCGCATGAA	891
O	1276	ctacaggaaggatgttcgtgtaactcttgaanaacggaatgttccttgcgaaggaattatgltccg	1335
D	892	TTGAAGATGAGCGTGCATCTTGAANAATAGAGTTGCACCTTGCTCAACGTCCTTTTCCA	951
O	1336	atggaagcaagatagtaacatgatatgtctcaagtgatggaacttggaaattaaactg	1395
D	952	ACGGAGGACACAAAGCTGCATAAGGAGATCGCGGAATATGAAGGAACATGTGAGTTCTTAATG	1011
O	1396	ggctcgttgtaaatccaactc--ctgaagaagcaacggaacacgttgatctaaatga	1452
D	1012	ACTAGCCTCGAGCTGCACGCTTCACCTTGTAACAGAGAAACATCACCGGCTTAAAGTA	1071
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D	1072	GCACCTTTCAAGATCTTAAGAAAGACATCAAAAGTAGACTTAAAGCCGCTTTTAAACCGTG	1131
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D	1132	GAACTCGGGAACGATTCCTCCGCGCTGTGGCAGTGTGTGCACCAAGTTATGAA	1187

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RESULT 11
US-08-989-478-15
; Sequence 15, Application US/08989478
; Patent No. 5986082
;
GENERAL INFORMATION:
;
APPLICANT: Uknes, Scott
;
APPLICANT: Hunt, Michelle
;
APPLICANT: Steiner, Henry-York
;
APPLICANT: Ryals, John
;
TITLE OF INVENTION: ALTERED FORMS OF THE NIMI GENE CONFERRING
;
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
;
NUMBER OF SEQUENCES: 32
;
CORRESPONDENCE ADDRESSES:
;
ADDRESSEE: No. 5986082artis Corporation

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DB 697 CATGTTGCTGAGATGCGGAG 756  
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## RESULT 13

US-08-989-478-1

Sequence 1, Application US/08989478

Patent No. 5986082

GENERAL INFORMATION:

APPLICANT: Uknes, Scott

APPLICANT: Hunt, Michelle

APPLICANT: Steiner, Henry-York

APPLICANT: Ryals, John

TITLE OF INVENTION: ALTERED FORMS OF THE NIM1 GENE CONFERRING

NUMBER OF SEQUENCES: 32

DISEASE RESISTANCE IN PLANTS

CORRESPONDENCE ADDRESS:

ADDRESS: No. 5986082artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: No. 5986082th Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,478

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/033,177

FILING DATE: 13-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,379

FILING DATE: 27-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,382

FILING DATE: 27-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,730

FILING DATE: 10-JAN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/035,021

FILING DATE: 10-JAN-1997

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/035,022

FILING DATE: 10-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: PF/5-21214/P1/CGC1911

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5655 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: exon

LOCATION: 2787..3347

OTHER INFORMATION: /product= "1st exon of NIM1"

FEATURE:

NAME/KEY: exon

LOCATION: 3427..4162

OTHER INFORMATION: /product= "2nd exon of NIM1"

FEATURE:

NAME/KEY: exon

LOCATION: 4271..4474

OTHER INFORMATION: /product= "3rd exon of NIM1"

FEATURE:

NAME/KEY: exon

LOCATION: 4586..4866

OTHER INFORMATION: /product= "4th exon of NIM1"

FEATURE:

NAME/KEY: CDS

LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)

US-08-989-478-1

## Query Match

Best Local Similarity 12.7%; Score 258.4; DB 2; Length 5655;

Matches 455; Conservative 0; Mismatches 291; Indels 12; Gaps 1;

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APPLICATION NUMBER: US 60/035,021
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,022
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/035,024
FILING DATE: 10-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/875,015
FILING DATE: 16-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: P/5-21215/P1/CGC1912
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5655 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: exon
LOCATION: 2787..3347
OTHER INFORMATION: //product= "1st exon of NIM1"
FEATURE:
NAME/KEY: exon
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OTHER INFORMATION: //product= "4th exon of NIM1"
FEATURE:
NAME/KEY: CDS
LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)
US-08-996-685-1

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RESULT 15  
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 Sequence 2, Application US//08880179  
 Patent No. 6091004  
 GENERAL INFORMATION:  
 APPLICANT: Ryals, John  
 APPLICANT: Delaney, Terry  
 APPLICANT: Friedrich, Leslie  
 APPLICANT: Weymann, Kristianne  
 APPLICANT: Layton, Kay  
 APPLICANT: Ellis, Daniel  
 APPLICANT: Uknes, Scott  
 APPLICANT: Jesse, Taco  
 APPLICANT: Vos, Pieter  
 TITLE OF INVENTION: GENE ENCODING A PROTEIN INVOLVED IN THE  
 TITLE OF INVENTION: SIGNAL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED RESIS  
 TITLE OF INVENTION: IN PLANTS  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 6091004artis Corporation  
 STREET: 520 White Plains Road, P.O. Box 2005  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10591  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/880,179  
 FILING DATE:  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: CGC 1909  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 541-8587

TELEFAX: (919) 541-8689  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5655 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHEetical: NO  
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 LOCATION: 4586..4866  
 OTHER INFORMATION: /product= "4th exon of NIM1"  
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 NAME/KEY: CDS  
 LOCATION: join(2787..3347, 3427..4162, 4271..4474, 4586..4866)  
 US-08-880-179-2

Query Match 12.7%; Score 258.4; DB 3; Length 5655;  
 Best Local Similarity 60.0%; Pred. No. 4.6e-47;  
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 Job time: 6285 sec

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